RESULT 3 ABB38848

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Gaps

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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-tich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the derived oligopeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                 Human, PRP-1; proline-rich protein; saliva; dental caries;
chromosome 12p13.2; arginine catabolism; ammonia production; pH increase;
oral bacterium; caries prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New oligopeptides comprising 2 arginine residues from degradation proline-rich proteins, useful for preventing dental caries.
                                                                                                                                                                                                                                                                                                                                                    Human saliva PRP-1 fragment (residues 99-115), SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 62; DB 4; Length 17; 100.0%; Pred. No. 0.037; tive 0; Mismatches 0; Indels
                                                               100.0%; Score 62; DB 4; Length 10; 100.0%; Pred. No. 0.023; ive 0; Mismatches 0; Indels
derived oligopeptides of the invention
                                                                                                                                                                                                                                                   AAB48783 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 24; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-2000; 2000WO-SE000930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99SE-00001773
                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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                                                              Ouery Match
Best Local Similarity 100
Matches 10; Conservative
                                                                                                                                 1 GGHPRPPRGR 10
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JOHANSSON I.
                                                                                                                                                                 1 GGHPRPPRGR
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                                 Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stroemberg N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                     09-MAR-2001
                                                                                                                                                                                                                                                                                     AAB48783;
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                                                                                                                                                                                                                   RESULT 2
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #6360 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                 Human; foetal liver; gene expression; single exon nucleic acid probe
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0
                                                                                     Peptide #6354 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 31483; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 62; DB 4; Length 132; 100.0%; Pred: No. 0.23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM32323 standard; protein; 132 AA
ABB38848 standard; peptide; 132 AA.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000669
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                                                        (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGHPRPPRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 132 AA;
                                                                                                                                                                           WO200157277-A2.
                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-0CT-2001
                                                          04-FEB-2002
                                                                                                                                                                                                         09-AUG-2001
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                             ABB38848;
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Gaps

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 31599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human brains.
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                                                                                                                                                                                  Example 4; SEQ ID NO 32364; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 62; DB 4; Length 132; 100.0%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                  Chen W, Rank DR;
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-006324687P.
27-SEP-2000; 2000US-0234687P.
27-CEP-2000; 2000US-0234589P.
                (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
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Best Local Similarity 100.
Matches 10; Conservative
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                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 GGHPRPPRGR
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                                                                                  WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                           Sequence 132 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP: see AAI31115-AAI57546). The present sequence is a peptide encoded by one such probe in the probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM72058 standard; protein; 132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression in human placenta.
                                                                                                                                              04-FEB-2000; 2000US-0180312P.
26-MN-22000; 2000US-0207456P.
30-UUN-2200; 2000US-0060840B.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456F.
30-UJN-2000; 2000US-0060408
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-023468TP.
04-OCT-2000; 2000GB-00024263.
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                                                                                                              30-JAN-2001; 2001WO-US000663
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es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 132 AA;
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                                    WO200157272-A2
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Homo sapiens
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                                                                        09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                           SG,
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Best Loc Matches

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RESULT 5

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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis.

The principle cornary heart disease. ABG47346-ABG5930 represent human sasciated with cornary heart disease. ABG47346-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful for analyzing
which may enable the diagnosis and improved treatment of nervous system diseases such as Alzhainer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
                                                                                                                      Score 62; DB 4; Length 132;
Pred. No. 0.23;
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0
                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 32390; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human liver peptide, SEQ ID No 32390.
                                                                                                                                                                                                                                                                                                                  ABG53742 standard, peptide, 132 AA.
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                                                                                                                        100.0%;
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21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-00608408.
2000US-00632366.
2000US-0234687P.
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                        Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                             1 GGHPRPPRGR 10
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                                                                                       Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                            RESULT 7
ABG53742
                                                                                                                                                                                                                                                                                                                  8833333
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Sequence 132 AA,

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12187 open reading frames derived from human lung, omprising den expression in a sample carid expressed in the human lung, measuring gene expression in a sample cellection of detectably labeled nucleic acids derived from human lung man, and (b) measuring the label detectably bound to each probe of the array, identifying exons in a eukaryotic genome, comprising (a) and prithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably aloning from the eukaryote; and (b) detecting specific hybridisation of detectably having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene,
                                                                                                                                                                                                                                                                                                                                 Human peptide encoded by genome-derived single exon probe SEQ ID 31538.
                                                                                                                                                                                                                                                                                                                                                                                         chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis, neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; Niemann-Pick disease; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                             Human, single exon probe, asthma, lung cancer, COPD, ILD,
chronic obstructive pulmonary disease; interstitial lung disease;
                                             .;
0
100.0%; Score 62; DB 4; Length 132; 100.0%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          measure gene expression in human lung samples.
                        Pred. No. 0.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 31538; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                                                                                                        ABG41873 standard; peptide; 132 AA.
                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0180312P.
2000US-0207456P.
2000US-00608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000665
                                                                                                                                                                                                                                                                                                  (first entry)
        Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                      2
                                                                                                                         90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-114183/15
                                                                                      1 GGHPRPPRGR
                                                                                                                         81 GGHPRPPRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200186003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FBB-2000;
                                                                                                                                                                                                                                                                                                    19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L5-NOV-2001
                                                                                                                                                                                                                                                                 ABG41873;
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comprising (a) identifying exone from genomic sequence by the method
above and (b) measuring the expression of each of the exons in several
tissues and/tor cell types using hybridisation to a single exon
microarrays having a probe with the exon, where a common pattern of
expression of the exons in the tissues and/or cell types indicates that
the exons should be assigned to a single gene, a peptide comprising one
of 12011 sequences, mentioned in the specification, or encoded by the
probes/open reading frames (ORF). The probes are used for gene expression
analysis, and for identifying exons in a gene, particularly using human
lung derived mRNA and for the study of lung diseases such as asthma, lung
cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
tuberous sclerosis, gaucher's disease, Niemann-Pick disease, Hermansky-
Pudlak syndrome, garcoidosis, pulmonary haemosiderosis, pulmonary
histiocytosis, lymphangioleiomyomntosis, primary ciliary
dyskinesis, pulmonary hypertension and hyaline membrane disease. The
present sequence is a peptide/protein encoded by a single exon probe of
the invention. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pot_equences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 132 AA;
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                                                       Gaps
                                                    6
Query Match 100.0%; Score 62; DB 5; Length 132; Best Local Similarity 100.0%; Pred. No. 0.23; Matches 10; Conservative 0; Mismatches 0; Indels
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1 GGHPRPPRGR 10 90 GGHPRPPRGR 임 ABR57423 standard; protein; 149 AA.

15-SEP-2003 (first entry)

ABR57423;

Human NOV7 protein SEQ ID NO:24.

Human; NOVX; cytostatic; cardiant; antiinflammatory; immunosuppressive; antiallergic; haemostatic; anti-HV; antidiabetic; antiarteriosclerotic; ancretic; antiartherio; nephrotropic; antiarthitic; hepatotropic; neuroprotective; noctropic; antibacterial; virucide; antiparasitic; relaxant; anticonvulsant; hypotensive; vasotropic; antiparasitic; vulneraxy; antiogenic; antiangiogenic; gene therapy; vaccine; cancer; cardiomyopathy; atherosclerosis; hypetrension; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma; acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis; Alzheiner's disease; Parkinson's disease; goitre; infection; stroke; muscular dystrophy; epilepsy; wasting disorder; chromosome 12. ABES 7423

ABES 7423

ID ABES 7423

XX

XX

XX

XX

DT 15-6

XX

Hume

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Homo sapiens.

WO200294870-A2

28-NOV-2002.

02-NOV-2001; 2001WO-US051580

02-NOV-2000; 2000US-0245291P. 02-NOV-2000; 2000US-024517P. 07-NOV-2000; 2000US-0246612P. 08-NOV-2000; 2000US-0246871P. 26-DAN-2001; 2001US-0264389P. 26-DAN-2001; 2001US-0264339P. 29-JAN-2001; 2001US-026439P.

(CURA-) CURAGEN CORP

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ACFO3547 to ACFO3570 encode the human NOVX proteins (1) given in ABR57412 to ABR57435. (1) have cytostatic, cardiant, antiinflammatory, nootropic, immunosuppressive, antializeric, anticomplex, antializeric, anticomplex, immunosuppressive, antializeric, anticonvolant, hypotensive, antibacterial, relaxant, antiarthritic, hepatotropic, neuroprotective, antibacterial, relaxant, vulnerary, angiogenic antianglogenic activities, and can be used in vulnerary, angiogenic and antianglogenic activities, and can be used in contermine the presence or absence of (1) in a sample. The NOVX polypeptides and their antibodies can be used to determine the presence or absence of (1) in a sample. The NOVX polypeptides, polymucleotides encoding them, and antibodies against them, are useful in manufacturing a medicament for treating or preventing a reuseful in manufacturing a medicament for treating or preventing a syndrome associated with a NOVX-associated disorder such as hypertension, cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation, autoimmundeficiency syndrome (ADDS), immunoglobulin (Ig) A nephropathy, climtosis, arthitis, Alzheimer's disease, Parkinson's disease, goite, iffections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. ACF03571 to ACF03644 repersent PCR primers and probes for NOVX construction.
                                                                                                                                                                                                             New NOVX polypeptide useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.
MA, Macdougall JR, Smithson G, Millet I, Stone DJ;
E, Ellerman K, Alsobrook JP, Lepley DM, Burgess CE;
A, Edinger SR, Gangolli EA, Gorman L, Taupier RJ, Li,
Fernandes ER, Vernet CAM, Tchernev VT, Casman SJ, Shenoy S;
I, Furtak K, Baumgartner JC, Colman SD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Length 149;
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Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                   Claim 1; Page 69; 346pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGHPRPPRGR 10
                                                                                              Mishra V, Furtak K,
                                                                                                                                               WPI; 2003-140359/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 149 AA;
                                                                                                                                                                         N-PSDB; ACF03558
                            Gunther E,
Spytek KA,
     Grosse WM,
                                                                            Guo X,
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Human secreted protein SECP-44 SEQ ID NO:44. ABR56769 standard; protein; 154 AA. (first entry) GGHPRPPRGR 107 30-JUL-2003 ABR56769;

Human, secreted protein, SECP, cytostatic, antiarteriosclerotic, anticonvulsant, nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic, antiinflammatory, thyromimetic, gene therapy, cancer, cell proliferative disorder, thyromizelerosis, neurological disorder; epilepsy, Huntington's disease, stroke, immune disorder, allergy, AIDS, inflammatory disorder, developmental disorder; hypothyroidism; Cushing's syndrome; infection. W02003016506-A2. Homo sapiens 27-FEB-2003.

15-AUG-2002; 2002WO-US027143

vaccine.

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ARCT9026 to ARR56805, designated SECP-1 to SECP-80. SECP sequences can ARR56726 to ARR56805, designated SECP-1 to SECP-80. SECP sequences can have overceating, antiarterior cartionistic, antiariant, antialiammatory, nootropic, neuroprotective, cerebrotic, antianilammatory, notropic, neuroprotective, cerebrotic antianilammatory, correcting and polymucleotides can be used in dagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of SECP, such as call proliferative (e.g. expression or overexpression of SECP, such as call proliferative (e.g. cancer, atheroscierosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AlDS, allergies) and disease, stroke), immune/inflammatory (e.g. AlDS, allergies) and compounds on the expression of mucleic acid and amino acid sequences of SECP. The SECP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human, marker, expressed sequence tag, EST; arabidopsis, tumour, stress-induced phenotype, hyperosmotic stress; colon cancer, immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human secreted proteins (SECP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant SECP expression e.g. cancer, AIDS, atherosclerosis, Huntington's disease, stroke, infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                        Tang TY, Warren BA, Gietzen KJ, Lal PG, Yue H, Honchell CD; Lehr-Mason PM, Burford N, Xu Y, Baughn MR, Duggan BM, Tran UK; Lee EA, Forsythe IJ, Richardson TW, Lee S, Thangavelu K, Yue H; Emerling BM, Walia NK, Azimzai Y, Sanjanwala B, Haila AJA; Berowsky ML, Nguyen DB, Ison CH, Astromoff A, Ding L, Lee SY; Becha SD, Ramkumar J, Gandhi AR, Jin P, Fu GK, Swarnakar A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 62; DB 6; Length 154; 100.0%; Pred. No. 0.27; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA83798 standard; protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 222; 286pp; English.
                                                   2001US-0317824P.

2001US-0324040P.

2001US-034380F.

2001US-034229P.

2002US-0357002P.

2002US-0362439P.

2002US-036641P.
2001US-0313249P.
2001US-0314752P.
2001US-0317818P.
                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC.
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Query Match
Best Local Similarity 100.v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 GGHPRPPRGR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ACC79069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 154 AA;
                                                                          21-SEP-2001;
24-SEP-2001;
02-NOV-2001;
28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
                                         37-SEP-2001;
                                                         37-SEP-2001;
                                                                                                                                                                   06-MAR-2002;
                                                                                                                                                                                 19-MAR-2002;
                                                                                                                                                                                                        30-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
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The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed in the phenotype/cell type of interest tith all ESTB known to be expressed in the phenotype/cell type of interest that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably care tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon content in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is come in a human, for detecting a tumour cell. An antibody of the invention is content in a human, for detecting a tumour cell. An antibody of the invention is content in a human, for detecting a tumour cell. An antibody of the invention is content in the presence of peptides encoded by the invention for a tumour associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a cumour associated antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; salivary acidic proline-rich phosphoprotein; PRP; autoantigen, atopic dermatitis-inducing protein; salivary gland; IgE autoantibody; immunoglobulin E; mast cell activation; basophil activation; diagnosis; risk assessment; sensitisation remedy; dermatological; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                        Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
                                                                                                                                                                                                                                                                                                                       Lobashev AV, Krukovskaya LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human salivary acidic proline-rich phosphoprotein (PRP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                           Kozlov AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 29; Page 191-192; 516pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC98216 standard; protein; 166 AA.
                                                                                                                                                                                                    30-MAY-2001; 2001US-029399P.
                                                                                                                                                                                                                   22-OCT-2001; 2001US-0330457P.
                                                                                                                                                            30-MAY-2002; 2002WO-IB004189
                                                                                                                                                                                                                                                                                                                             Baranova AV, Yankovsky NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-2004 (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                     (BIOM-) BIOMEDICAL CENT
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N-PSDB; ADA83797.
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                                                                               WO2002103028-A2
                                         Homo sapiens.
                                                                                                                    27-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue.
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ADC98216
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us-10-009-709-7.rag

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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are fegraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAS48771-B48783 represent the PRP-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                      Claim 4; Page 24; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167
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11-MAY-2000; 2000WO-SE000930
                                           17-MAY-1999; 99SE-00001773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Query Match
Best Local Similarity 100.v.
Post 9; Conservative
                                                                                                                                                              Stroemberg N, Johansson I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                        STROEMBERG N.
JOHANSSON I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHPRPPRGR 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
                                                                                                                                                                                                          WPI; 2001-031923/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS93083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2001.
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                                                                                                              (JOHA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the human atopic dermatitis-inducing proteins, salivary acidic proline-rich phosphoprotein (RRP; ADC9816) and prolactin-inducible protein (FPP; ADC98118), and their post-translationally modified forms. These proteins are secreted by salivary or sweat glands and bind to IgE autoantibodies, thereby activating mast cells and basophils. The invention also relates to antigenic peptide fragments of RPP or PIP, antibodies which bind to PRP or PIP, methods for diagnosing atopic dermatitis by determining whether an individual is at risk of developing atopic dermatitis by determining the presence of PRP- or PIP-specific antibodies or immune complexes, or by quantifying histamine release; and sensitisation remedies for atopic dermatitis containing PRP and/or PIP or their peptides as the active ingredient. PRP, PIP and their antibodies are useful in diagnosing atopic dermatitis. They whether an individual is at risk of developing atopic dermatitis. They are also useful in developing sensitiation remedies for the treatment of atopic dermatitis. The present sequence represents the specifically atopic dermatitis. They are also useful indeveloping sensitiation remedies for the treatment of atopic dermatitis. They resent sequence represents the specifically atomic dermatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Atopic dermatitis-inducing proteins, applicable in diagnosis of including risk of onset, and in developing sensitization remedies for the disease.
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chromosome 12p13.2; arginine catabolism; ammonia production; pH increase;
oral bacterium; caries prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 62; DB 7; Length 166; 100.0%; Pred. No. 0.28; o. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      Koro O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 2; 43pp; Japanese.
                                                                                                                                                                                                                                                                          (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB48778 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                   Tanaka T,
                                                                                                                                                                                                                               08-APR-2002; 2002JP-00105425.
                                                                                                                                                                                 04-APR-2003; 2003WO-JP004325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 GGHPRPPRGR 124
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                                                                                                                                                                                                                                                                                                                   Hide M, Yamamoto S,
                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-833567/77.
N-PSDB; ADC98215.
  antiinflammatory.
                                                                                           WO2003084991-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 166 AA;
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                                                Homo sapiens,
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Matches

RESULT 13 AAB48778

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AAB48779 standard; peptide; 8 AA. 17-MAY-1999; RESULT 15 AAB48779

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recardion (PCR) primares, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders olypeptide and polymucleotide sequences have applications in dispostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biddiversity amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 59255; 103pp; English.
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Sequence 843 AA;

ö Query Match 82.3%; Score 51; DB 4; Length 843; Best Local Similarity 100.0%; Pred. No. 42; Matches 8; Conservative 0; Mismatches 0; Indels

AAB48779;

09-MAR-2001 (first entry)

Human saliva PRP-1 fragment (residues 101-108), SEQ ID NO:9.

Human, PRP-1; proline-rich protein, saliva; dental caries; chromosome 12p13.2; arginine catabolism; ammonia production; pH increase; oral bacterium; caries prevention.

Homo sapiens

WO200069890-A1.

23-NOV-2000.

11-MAY-2000; 2000WO-SE000930.

(STRO/) STROEMBERG N.

(JOHA/) JOHANSSON I.

Stroemberg N, Johansson I;

New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.

Claim 4; Page 24; 36pp; English.

ABB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12pl3.2 and are potential determinants of a person's succeptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the derived oligopeptides of the invention The invention relates to human PRP-1-derived oligopeptides (AAB48771-

Sequence 8 AA;

ö 80.6%; Score 50; DB 4; Length 8; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 8; Conservative

3 HPRPPRGR 10

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Search completed: April 6, 2004, 16:06:39 Job time : 56.9813 secs

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Sequence 43644, A Sequence 80, Appl Sequence 10259, A Sequence 1087, A Sequence 14087, A Sequence 43478, A Sequence 223703, Sequence 2787, Appl Sequence 2787, Appl Sequence 2787, Appl Sequence 2787, Appl Sequence 2488, Appl Sequence 1418, Appl Sequence 1418, Appl Sequence 45389, A Sequence 45389, A Sequence 45389, A Sequence 45389, Appl Sequen
                                                                                                                                                                                                                         April 6, 2004, 16:14:50; Search time 39.2523 Seconds (without alignments) 66.909 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_MBW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NBW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NBW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-84 846A-6

US-09-815-242-100259

US-09-815-242-14087

5 US-10-84-846A-7

2 US-10-425-114-69167

2 US-10-425-114-69167

2 US-10-425-114-69167

2 US-10-424-599-223703

US-10-424-599-274737

2 US-10-424-599-250895

5 US-10-374-761-45389

US-09-864-761-45389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1071772 segs, 262633353 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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326
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WW424W02W000000000 - 4 44040404	Sequence 114, App
US-10-424-599-233437 US-10-425-114-50588 US-10-425-114-60148 US-10-425-114-60168 US-10-425-114-48471 US-10-425-114-48471 US-10-425-114-7314 US-10-425-114-7314 US-10-425-114-7314 US-10-425-114-7314 US-10-425-114-64280 US-10-424-599-192615 US-10-425-114-64280 US-10-425-114-64280 US-10-425-114-64280 US-10-112-944-336 US-10-112-944-336 US-10-112-944-336 US-10-112-187-35 US-10-282-1227-63880 US-10-282-1227-63880 US-10-282-1227-63880 US-10-282-1227-63880 US-10-282-1227-63880	
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	1.99
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11111222222222222222222222222222222222	4.45

ALIGNMENTS

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JS-09-864-761-43644
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; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1. US-10-084-846A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.4%; Score 48; DB 15; Length 19662; 80.0%; Pred. No. 2.8e+03; tive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Obligation, Kari L.
APPLICANT: Obligation, Kari L.
APPLICANT: Apskind, Judith W.
APPLICANT: Wall, Wall, Woldith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: 1000-03-21
CURRENT PELLORITON NUMBER: 60/19,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: 60/200,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PELLORITON NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELLING DATE: 2000-12-22
PRIOR PELLING DATE: 2000-12-22
PRIOR PELLOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR PELLOR PELLOR NUMBER: 60/259,308
PRIOR PELLOR PELLOR NUMBER: 60/250,308
PRIOR PELLOR PELLOR NUMBER: 60/269,308
                                                                                       APPLICANT: MUHLENWEG, AGNES
APPLICANT: TREFZER, AXEL
APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILANYCIN DERIVATIVES
FILE REFERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: PCT/EP01/09815
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
STORMER OF SEQ ID NOS: 120
SOFTWARE: PATENTIN VET. 3.2
SOFTWARE: PATENTIN VET. 3.2
SOFTWARE: PATENTIN VET. 3.2
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SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 10259
LENGTH: 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10259, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                              APPLICANT: WEITNAUER, GABRIELE
APPLICANT: MUHLENWEG, AGNES
APPLICANT: TREFZER, AXEL
   US20040006026A1
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYPE: PRT
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APPLICANT: Baranova, A. V.
APPLICANT: Yankovsky, N. K.
APPLICANT: Yankovsky, N. K.
APPLICANT: Krokovsky, N. V.
APPLICANT: Krokovsky, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences FILE REFERENCE: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: Petentin version 3.1
SEQ ID NO 80
LENGTH: 166
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ORGANISM: Homo sapiens
FATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.35
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BADIT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BARIN, SIGNAL = 0.35
OTHER INFORMATION: SYPESSED IN BASIN, SIGNAL = 0.77
OTHER INFORMATION: SYPESSED IN BASIN, SIGNAL = 0.77
OTHER INFORMATION: SYPESSED IN BASIN, SYPENDE 1.00e-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 62; DB 9; Length 132;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 10; Conservative 0; Mismatches 0; Indels
          FRIOR FILLING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00661
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PELING DATE: 2001-01-30
PRIOR FILLING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2001-01-29
PRIOR FILLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43644
LENGTH: 132
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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US-10-084-846A-6
; Sequence 6, Application US/10084846A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 GGHPRPPRGR 124
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CRGANISM: Homo sapiens
US-10-157-031-80
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Sequence 69167, Application US/10425114

Sequence 69167, Application No. US20040034888A1

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Screen. Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Back IS Screen E

APPLICANT: Back IS Screen E

APPLICANT: AD INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
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APPLICANT: Liu, Jingdong
APPLICANT: Exou, Yihua
APPLICANT: Screen, Steven B
APPLICANT: Green, Steven B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 2.; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2. US-10-084-846A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17307C10_FLI.pep
US-10-425-114-69167
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
FRIOR PRILOR APPLICATION NUMBER: PCT/EP01/09815
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO.
SEQ ID NO.
                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Streptomyces viridochromogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2258 GTPRPPRGR 2266
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ORGANISM: Zea mays
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LENGTH: 238
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                                                                Gaps
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APPLICANT: Oblean, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Yamancho. Robert T.
APPLICANT: Yamancho. Robert T.
APPLICANT: Yamancho. Robert T.
APPLICANT: Yamancho. Robert T.
APPLICANT: Xu, H. Howa R.
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 100-11A
CURRENT ELITED OF INVENTION: 2001-03-21
FILE REFERENCE: ELITEA. 011A
CURRENT APPLICATION NUMBER: 60/201,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 14087
LUNCH AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.2%; Score 46; DB 9; Length 326; 77.8%; Pred. No. 1.4e+02;
     Score 46; DB 9; Length 326;
Pred. No. 1.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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Publication No. US20040006026A1
GENERAL INFORMATION:
APPLICANT: WEITHAUER, GABRIELE
APPLICANT: TREFZER, ARES
APPLICANT: BECITHOLD, ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)...(326)
CTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-14087
                                                                                                                                                                                                                                                                                                        Sequence 14087, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
           Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 GGRPRPPKG 262
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                                                                                                                   1 GGHPRPPRG 9
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                                                                                                                                                                                                                                                                                 -09-815-242-14087
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APPLICANT: Lass Thomas J
APPLICANT: Assa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Alou Yihua
APPLICANT: Alou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 274737
LENGTH: 123
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                                                                                                             Gaps
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                                                                      Length 707;
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  ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 2457215CD1
US-09-919-039-278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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US-10-424-599-274737
                                                                      Score 43.5; DB 10;
Pred, No. 6e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0;
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LOCATION: (1)..(185)
PERTURE INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(123)
PEATURE INFORMATION: unsure at all Xaa locations
PEATURE:
                                                                                                                                                                                                                                                                                 Sequence 274737, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                        70.2%;
                                                                          Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                          228 GGHPKPPHKG 237
                                                                                                                                                     1 GGHPRPP-RG 9
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ORGANISM: Glycine max
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15 GGHPKPP 21
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US-10-424-599-274737
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Publication No. US20440031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Arou Yihua
APPLICANT: Can Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 12032)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 223703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-09-919-039-278
JS-09-919-039-278
Sequence 278, Application US/09919039
Publication No. US20030108871A1
GENERAL INFORMATION:
TILLE REPERENCE: PA-0035 US
TILLE REPERENCE: PA-0035 US
CURRENT APPLICANT:
PRIOR APPLICANT:
PRIOR APPLICATION NUMBER: US/09/919,039
CURRENT FILING-DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR SEQ ID NOS: 401
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 401
SEQ ID NO 278
LENGTH: 707
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement PLE REFERENCE: 38-21(5313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 SEQ ID NOS: 73128 SEQ ID NO 43478
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                                                                                                                                                                                                                                                       Length 277;
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                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_44033C.1.pep
US-10-424-599-223703
                                                                                                                                                                                                                                                   Query Match
72.6%; Score 45; DB 12; 1
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: 700423863_FLI.pep
US-10-425-114-43478
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                                                                                                                                                                                                                                                                                                                                                                    86 HPRPPRG 92
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                                                                                                                                                       ORGANISM: Zea mays FEATURE:
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                                                                                                                                       TYPE: PRT
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OTHER INFORMATION: MAP TO APRO1427.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.75
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.55
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.61
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.61
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.61
OTHER INFORMATION: EXPLANDAN HIT: D15016, EVALUE 3.70e+00
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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APPLICANT: BIGHTM, FIRTHE E
APPLICANT: Dubell III, Arnold T
APPLICANT: Pineda, Omaira
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
ITILE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES IN PLANTS
ITILE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES IN PLANTS
ITILE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES IN PLANTS
ITILE REPRENCE: BIL - 004 - 107
FILE REPRENCE: RELIAND NUMBER: 09/837, 944
PRIOR APPLICATION NUMBER: 09/934, 455
PRIOR FILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-108-22
PRIOR PLILING DATE: 2001-11-19
PRIOR PLILING DATE: 2001-12-11
PRIOR PLILING DATE: 2001-12-11
PRIOR PLILING DATE: 2002-06-14
PRIOR PLILING DATE: 2002-06-14
PRIOR PLILING DATE: 2002-06-09
PRIOR FILING DATE: 2002-08-09
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Pred. No. 2.2e+02;
0; Mismatches 2; Indels
                                                                                                              Query Match 69.4%; Score 43; DB 12; Length 185; Best Local Similarity 70.0%; Pred. No. 2.2e+02; Matches 7; Conservative 1; Mismatches 2; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_68568C.1.pep
US-10-424-599-250895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCS-10-374-780A-1418
Sequence 1418, Application US/10374780A
PUBLICation No. US/20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jang,
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Orthologous to G1073
US-10-374-780A-1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Creelman, Robert A
Ratcliffe, Oliver
Adam, Luc J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.4%;
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                160 GGPPRPPAGK 169
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ORGANISM: Zea mays
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RESULT 15
US-10-424-599-149900

is Sequence 149900, Application US/10424599

sequence 149900, Application US/10424599

publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Covaria David K

APPLICANT: Toou Yibna
APPLICANT: Covaria David K

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 149900

LENGTH: 229

CURRENT: Covaria David M

SEQ ID NO 149900

LENGTH: Covaria David M

SEQ ID NO 149900

CORTER INFORMATION: Unsure at all Xaa locations

FEATURE:
NAME/KEY: Unsure

COTHER INFORMATION: Clone ID: PAT_MRT3847_106381C.1.pep
31 GHRRPPRG 38
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Search completed: April 6, 2004, 17:05:59 Job time: 44.2523 secs

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Query Match 67.7%; Score 42; DB 12; Length 229; Best Local Similarity 70.0%; Pred. No. 3.5e+02; Matches 7; Conservative 1; Mismatches 2; Indels

Page

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us-10-009-709-7.rapm

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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Database

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Sequence 17988, A Sequence 13405, A Sequence 13405, A Sequence 31592, A Sequence 31594, A Sequence 31594, A Sequence 31592, A Sequence 31592, A Sequence 24, Appli Sequence 13417, A Sequence 13417, A Sequence 62326, A Sequence 62326, A Sequence 62326, A Sequence 62326, A Sequence 6326, A Appli Sequence 61226, A Appli Sequence 61226, A Appli Sequence 6122, Appli Sequence 61226, A Appli Sequence 6122, Appli Sequence 612, Appli Sequence 612, Appli Sequence 142, Appli Sequence 1159, Appli Mappli M
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Sequence 650, App
Sequence 650, App
Sequence 16373, A
Sequence 16373, A
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Sequence 406, App
Sequence 8, Appli
Sequence 16601, A
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Sequence 8394, A
Sequence 49, Appl
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S US-10-009-709-7
S US-10-009-709-13
US-09-913-3
US-09-914-366-13405
US-09-914-366-13405
US-09-914-366-13405
US-09-914-366-13405
US-06-107-873-13405
US-10-102-99-31599
US-10-103-138-31538
US-10-103-138-31538
US-10-203-138-31538
US-10-203-138-313417
US-09-349-016-6709
US-10-002-945-88
US-10-002-945-88
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US-10-002-945-88
US-10-002-945-88
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US-10-002-945-88
US-10-003-949-116601
US-09-340-116601
US-09-340-116601
US-09-340-116601
US-09-343-366-16601
US-09-383-366-16601
US-09-383-366-16601
US-09-383-366-16601
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APPLICANT: Stromberg, Nicklas
APPLICANT: Ingegerd, Johansson
TITLE OF INVENTION: PREVENTION OF DENTAL CARIES
FILE REFERENCE: P/2432-44
CURRENT APPLICATION NUMBER: US/10/009,709
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: PCT/SE00/00930
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-009-709-7; Sequence 7, Application US/10009709; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-10-009-709-7
                                                                                                                 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                        6, 2004, 16:06:50; Search time 208.411 Seconds (without alignments) 46.833 Million cell updates/sec
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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62
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Ouery Match 100.0%; Score 62; DB 23; Length 131; Best Local Similarity 100.0%; Pred. No. 5; Matches 10; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 62; DB 33; Length 128; 100.0%; Pred, No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
APPLICANT: Bejanin, Stephane
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Jobert, Severin
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERRENCE: 81.031.PNO
CURRENT FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 17988
IEBNGTH: 128
TYPE: PPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13405, Application US/09834366
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Johert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPRENCE: B. 1.05. REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT PILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/197,873
PRIOR PLING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 13405
LENGTH: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SIGNAL
LOCATION: -16...1
NAME/KEY: UNSURE
LOCATION: 100
CATION: 100
OTHER INFORMATION: Xaa = Ala, Asp, Gly, Val
US-60-197-873-17988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SIGNAL
LOCATION: -16..-1
NAME/KEY: UNSURE
LOCATION: 33
OTHER INFORMATION: Xaa = Ala, Pro
NAME/KEY: UNSURE
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CIHER INFORMATION: Xaa = Asp, Asn
US-09-834-366-13405
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Best Local Similarity 100.
Matches 10; Conservative
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100.0%; Pred. No. 0.76;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17988, Application US/09834366
GENERAL INFORMATION:
APPLICANT: Bejanih, Stephane
APPLICANT: Bejanih, Stephane
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Johert, Severin
STERREN APPLICANTON NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
LENGTH: 128
                                                                                                                                                                                                                                                                           APPLICANT: Stronberg, Nicklas
APPLICANT: Stronberg, Nicklas
APPLICANT: Stronberg, Johansson
TITLE OF INVENTION: PREVENTION OF DENTAL CARIES
TILE REPERENCE: P/2432-44
CURRENT APPLICATION NUMBER: US/10/009,709
CURRENT PILING DATE: 2001-11-16
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 13
LENGTH: 17
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LOCATION: -16..-1
NAME/KEY: UNSURE
LOCATION: 100
OTHER INFORMATION: Xaa = Ala,Asp,Gly,Val
                                                                                                                                                                                                               US-10-009-709-13
; Sequence 13, Application US/10009709
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGHPRPPRGR 10
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                                                                                                               1 GGHPRPPRGR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 43644, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE REPERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: MAP TO AC006518.17
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EST HUMAN HIT: BF088785.1, EVALUE 1.00e-01
COTHER INFORMATION: SMISSPROT HIT: P02810, EVALUE 7.40e-02
PCT-US01-00663-32592
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 62; DB 1; Length 132; Best Local Similarity 100.0%; Pred. No. 5; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/190,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-
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       SEQ ID NO 32592
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APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chan, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR SITE REFERENCE: PB 0004 WO 7
CURRENT APPLICATION NUMBER: PCT/USO1/0063
CURRENT APPLICATION NUMBER: US 60/100/130
PRIOR APPLICATION NUMBER: US 60/20/456
PRIOR PILING DATE: 26 May 2000 (23.08.00)
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR PILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR PILING DATE: 32 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR PILING DATE: 32 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR PILING DATE: 30 June 2000 (30.06.00)
PRIOR APPLICATION NUMBER: US 60/200,600)
PRIOR APPLICATION NUMBER: US 60/200 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/200 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/200 (27.09.00)
PRIOR PILING DATE: 30 June 2000 (30.06.00)
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                                                                                                                            US-60-197-873-13405

US-60-197-873-13405

Sequence 13405, Application US/60197873

GENERAL INFORMATION:
APPLICANT: Bejanin Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Tanaka, Hiroaki
APPLICANT: Jobert, Severin
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yvea
FILE REFERENCE: 81.US1.PRO
CURRENT PRILIG DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 13405
LENGTH: 131

TYPE: PRT
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa = Ala, Pro
NAME/KEY: UNSURE
LOCATION: 50
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US-60-197-873-13405
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Best Local Similarity 100.
Matches 10; Conservative
115 GGHPRPPRGR 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SIGNAL
LOCATION: -16..-1
NAME/KEY: UNSURE
LOCATION: 33
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EXON NUCLEIC ACID PROBES USEFUL FOR
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                                                                                                                                                           Gequence 32364, Application US/10203134
GENERAL INFORMATION:
APPLICANT: Molecular Sharon General Sequence 32364, Application US/10203134
APPLICANT: Molecular Sharon General Sequence Depticant: Holecular Sequence 3.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: General Sequence DERIVED SINGLE EXON NUCLEIC ACID FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FOR TITLE OF INVENTION: HUMBER: US/01/203,134
CURRENT FILING DATE: 2002-09-02
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 05 May 2000 (26.05.00)
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR PELING DATE: 03 August 2000 (03.00.0)
PRIOR PELING DATE: 03 August 2000 (03.00.0)
PRIOR PELING DATE: 03 Cotcher 2000 (03.00.0)
PRIOR PELING DATE: 03 Cotcher 2000 (03.00.0)
PRIOR PELING DATE: 03 Octcher 2000 (03.00.0)
PRIOR PELING DATE: 03 Octcher 2000 (03.00.0)
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR FILING DATE: 2 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR FILING DATE: 30 June 2000 (30.06.00)
PRIOR PELING DATE: 30 June 2000 (30.06.00)
PRIOR PELING DATE: 30 June 2000 (30.06.00)
PRIOR PELING DATE: 30 June 2000 (30.06.00)
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR PELING DATE: 30 June 2000 (30.06.00)
PRIOR PELING DATE: 30 June 2000 (30.06.00)
PRIOR PELING DATE: 30 June 2000 (30.06.00)
PRIOR APPLICATION NUMBER: US 60/224,687
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC AC
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG
FILE REFERENCE: PB 0004 W0 S
CURRENT APPLICATION NUMBER: US/10/203,135
CURRENT FILING DATE: 2002-08-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: EST_HUMAN HIT: BF088785.1, EVALUE 1.00e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: SWISSPROT HIT: P02810, EVALUE 7.40e-02 US-10-203-134-32364
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PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
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Best Local Similarity 100.
Matches 10, Conservative
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81 GGHPRPPRGR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Reark, David R.
APPLICANT: Reark, David R.
APPLICANT: Reark, David R.
APPLICANT: Chen, Wensheng
ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL CURRENT APPLICATION NUMBER: US 60/10/102.993
CURRENT FILING DATE: 2002-08-02
PRIOR FILING DATE: 04 February 2000 (40.02.00)
PRIOR FILING DATE: 04 February 2000 (26.05.00)
PRIOR FILING DATE: 03 August 2000 (26.05.00)
PRIOR FILING DATE: 03 August 2000 (26.05.00)
PRIOR FILING DATE: 03 Cocober 2000 (33.00.00)
PRIOR FILING DATE: 03 Cocober 2000 (31.00.00)
PRIOR FILING DATE: 03 Cocober 2000 (27.09.00)
PRIOR FILING DATE: 21 September 2000 (27.09.00)
PRIOR FILING DATE: 21 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 30 September 2000 (30.00.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 30 September 2000 (30.00.00)
PRIOR APPLICATION NUMBER: US 60/608,408
PRIOR APPLICATION NUMBER: US 60/608,408
PRIOR PRIOR DATE: 30 September 2000 (30.00.00)
PRIOR APPLICATION NUMBER: US 60/608,408
PRIOR PRIOR PRIOR DATE: 30 September 2000 (30.00.00)
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                                                                                                  OTHER INFORMATION: MAP TO ACOO6518.17
OTHER INFORMATION: EXPRESSED IN PLACENIA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BARROW, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
US-09-864-761-43644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 62; DB 23; Length 132; Best Local Similarity 100.0%; Pred. No. 5; Matches 10; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 31599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31599, Application US/10182993 GENERAL INFORMATION:
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OTHER INFORMATION: MAP TO AC006518.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 10; Conservative
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ORGANISM: Homo sapiens
       TYPE: PRT
ORGANISM: Homo sapiens
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1 GGHPRPPRGR 10

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
FILE REFERENCE: PB 0004 WO.
CURRENT APPLICATION NUMBER: US/10/203,137
CURRENT FILING DATE: 2002-08-02
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                                                                                    EST_HUMAN HIT: BF088785.1, EVALUE 1.00e-01
                                                                                                                                                                                                                                                 Length 132;
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                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                  ), OTHER INFORMATION: SWISSPROT HIT: P02810, EVALUE 7.40e-02 US-10-203-136-32390
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
                                OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 38837
SOFTWARE: Molecular Dynamics Sequence Listing Engine
                                                                                                                                                                                                                                       100.0%; Score 62; DB 28;
11arity 100.0%; Pred. No. 5;
Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DAIRS: 2020-00-12
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,466
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR FILING DATE: 03 August 2000 (03.10.00)
PRIOR FILING DATE: 03 Cotober 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/234,667
PRIOR PILING DATE: 21 September 2000 (27.09.00)
PRIOR FILING DATE: 31 September 2000 (27.09.00)
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 38837
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Best Local Similarity 100.0%; Pred. No. 5;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 31483, Application US/10203139 ; GENERAL INFORMATION:
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OTHER INFORMATION: MAP TO AC006518.17
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Sequence 32592, Application US/10203137
GENERAL INFORMATION:
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Best Local Similarity
Matches 10; Conserva
                                                                 FEATURE:
OTHER INFORMATION:
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LENGTH: 132
                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 62; DB 28; Length 132; 100.0%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: SWISSPROT HIT: P02810, EVALUE 7.40e-02
US-10-203-135-31538
PRIOR APPLICATION NUMBER: US 09/652,366
PRIOR FILING DATE: 03 August 2000 (26.05.00)
PRIOR FILING DATE: 03 August 2000 (30.08.00)
PRIOR FILING DATE: 03 August 2000 (30.10.00)
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR FILING DATE: 37 September 2000 (27.09.00)
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR FILING DATE: 30 June 2000 (30.06.00)
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ.ID NOS: 37012
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ.ID NO 31538
LENGTH: 132
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SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 32390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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OTHER INFORMATION: MAP TO AC006518.17
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32390, Application US/10203136 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: MAP TO AC006518.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Molecular Dynamics, Inc. APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGHPRPPRGR 90
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: BaumgarLuch, Acadafayua
APPLICANT: BaumgarLuch, Steven D
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE SEPERBUCE: 2140-206
CURRENT APPLICATION NUMBER: US/10/002,945
CURRENT PILING DATE: 2001-11-02
PRIOR PILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-11-02
PRIOR PLING DATE: 2000-11-02
PRIOR PLING DATE: 2000-11-02
PRIOR PLING DATE: 2000-11-07
PRIOR PLING DATE: 2001-10-02
PRIOR PLING DATE: 2001-10-04
PRIOR PLING DATE: 2001-10-06
PRIOR PLING DATE: 2001-10-06
PRIOR PLING DATE: 2001-10-06
PRIOR PLING DATE: 2001-10-06
PRIOR PLING DATE: 2001-01-06
PRIOR PLING DATE: 2001-01-06
PRIOR PPLICATION NUMBER: 60/264,423
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 214
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                                         Mishra, Vishnu
Furtak, Katarzyna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 10; Conservative
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CORGANISM: Homo sapiens
US-10-002-945-24
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                                                                                           APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HANDAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HANDAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FILLE OF INVENTION: HANDAN GENOME EXPRESSION IN HUMAN FETAL LIVER
FILLE REFERENCE: PB 0004 WO 4
CURRENT APPLICATION NUMBER: US/10/203,139
CURRENT PILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,30
PRIOR PELING DATE: 04 February 2000 (34.00)
PRIOR PELING DATE: 05 May 2000 (26.05.00)
PRIOR PELING DATE: 03 August 2000 (33.08.00)
PRIOR APPLICATION NUMBER: US 60/234,56
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PELING DATE: 21 September 2000 (27.09.00)
PRIOR FILING DATE: 21 September 2000 (27.09.00)
PRIOR PELING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 37156
SOFTWARE: Molecular Dynamics Sequence Listing Engine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: EST_HUMAN HIT: BF088785.1, EVALUE 1.00e-01 FEATURE:
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OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.1
PEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/10002945 GENERAL INFORMATION:
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Gangolli, Esha A
Gorman, Linda
Taupier Jr, Raymond J
Molecular Dynamics, Inc.
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Bllerman, Karen
Alsobrook II, John P
Lepley, Denise M
Burgess, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xiaojia (Sasha
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7, Velizar
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                    Penn, Sharron G.
Rank, David R.
Hanzel, David K.
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Best Local Similarity 100
Matches 10; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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Gaps

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us-10-009-709-7.rai

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RESULT 2
US-09-252-991A-29452
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                                                                                                                                                          April 6, 2004, 15:56:34 ; Search time 14.6729 Seconds (without alignments) 35.185 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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-09-252-991A-30229
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-09-252-991A-32430
-09-489-039A-11696
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-09-252-991A-27041
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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62
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Match Length
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Perfect score:
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No.
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167	Sequence 4, Appli Sequence 4, Appli	ω',	۰, ۷	Sequence 6, Appli	φ,	Sequence 24713, A	26071,	Sequence 24516, A	_	Sequence 58, Appl	Sequence 1, Appli	Seguence 31760, A	Sequence 11, Appl
US-09-252-991A-16736 US-09-485-648-4	US-09-503-565-4 US-09-485-649-4	US-09-339-159B-8 US-09-485-648-2	US-09-503-565-2 US-09-485-649-2	US-09-339-159B-6	US-08-971-188-8	US-09-252-991A-24713	US-09-252-991A-26071	US-09-252-991A-24516	US-09-262-537-20	US-09-262-537-58	US-08-811-519-1	US-09-252-991A-31760	US-08-849-303-11
44	4 4	4.4	4 4	4	4	4	4	4	4	4	4	4	4
439 468	468 468	468 493	4 4 4 93	493	631	676	693	770	1466	1469	1471	1706	107
66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	64.5
4 4 1 1	41	41	41	4 4	41	41	41	41	41	41	41	47	40
28 29	30	3 B	3.4 4. R	3 6	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

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GENERAL INFORMATION:

Patent No. 6551795

GENERAL INFORMATION:

Patent No. 6551795

GENERAL INFORMATION:

AERUGINOSA FOR DAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 559
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Best Local Similarity 90.0
Matches 9; Conservative
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Sequence 22505, Application US/09252991A
; Sequence 22505, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: US/09/252,991A
; TITLE OF INVENTION: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29505
; SEQ ID NO 29505
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Sequence 32430, Application US/09252991A

Parent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 107196.118
FULLOR PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32430

LENGTH: 208
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APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERRENCE: 2709.2004001.
CURRENT APPLICATION NUMBER: US/09/489,039A
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Pred. No. 10;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Pseudomonas aeruginosa US-09-252-991A-29505
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Best Local Similarity
Matches 9; Conserv
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nes 8; Conserv
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Best Local S
Matches 8
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Sequence 31405, Application US/09252991A

Parent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE COF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31405
LIBRICH: 152
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107106.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1999-07-7
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17072
LENGTH: 223
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80.0%; Pred. No. 7.9;
Live 0; Mismatches 2; Indels
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                                                                    Length 418;
                                                                                                                  0; Indels
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                                                                    DB 4;
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Pred. No. 8.1;
0; Mismatches
                                                                  Score 50; DB 4; Pred. No. 7.6; 0; Mismatches
                                                                                                                                                                                                                                                                                                                               Sequence 17072, Application US/09252991A Patent No. 6551795
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US-09-252-991A-31405
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29452
                                                                    Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative 0
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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US-09-252-991A-31405
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US-09-252-991A-17072
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Sequence 17675, Application US/09252991A

Sequence 17675, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: MUCHEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17675

LENGTH 237
                                                                                                                                                                                                                                            Sequence 16715, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
PAPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16715
LENGTH: 690
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                               Gaps
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Pred. No. 82;
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                               2; Indels
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       77.8%; Pred. No. 56; tive 0; Mismatches
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US-09-252-991A-30229
; Sequence 30229, Application US/09252991A
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77.8%;
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Best Local Similarity 77.00
Best Local 7; Conservative
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Best Local Similarity 87.5-
7; Conservative
       Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                        270 GHPHPPDGR 278
                                                                              2 GHPRPPRGR 10
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US-09-252-991A-17675
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Patent No. 6551795
GSWERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: WCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REPRENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR SELING DATE: 1998-02-18
PRIOR SELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR SEQ ID NOS: 33142
SEQ ID NO 25573
LENGTH: 205
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEC ACID AND PIAGNOSTICS AND THERAPEUTICS

FILE REFERÊNCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: US 60/074,788

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO S. 33142

SEQ ID NO S. 20041
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                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                 Score 46; DB 4;
Pred. No. 22;
1; Mismatches
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11696
LENGTH: 331
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Patent No. 6551795
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US-09-252-991A-25573
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                                                                                                                                             TYPE: PRT; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11696
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 GGHARHPRGR 100
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US-09-252-991A-25573
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NUS-09-489-039A-8140

Sequence 8140
Sequence
                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09086168B
Patent No. 6638941
GENERAL INFORMATION:
APPLICANT: Castelhano, Arlindo
APPLICANT: Witter, David
TITLE OF INVENTION: TEMPLATES AND MODULATORS OF SH3 DOMAINS
FILE REFERENCE: 60384-B
CURRENT APPLICATION NUMBER: US/09/086,168B
CURRENT APPLICATION NUMBER: US/09/086,168B
CURRENT PILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 18
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Pred. No. 26;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 18;
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67.7%; Score 42; DB 4
Best Local Similarity 87.5%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches
Pred. No. 87;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: April 6, 2004, 16:19:40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE
LOCATION: (1)...(18)
CTHER INFORMATION: Synthetic Peptide
US-09-086-1688-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: SH3 test peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Klebsiella pneumoniae US-09-489-039A-8140
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Best Local Similarity 87.5%;
Matches 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                            121 GGRPRPPR 128
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US-09-086-168B-5
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                                     GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: ALERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PLILING DATE: 1999-02-18

PRIOR PLILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

ANDER OF SEQ ID NOS: 33142
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APPLICANT: VAN DEN HURK, SYLVIA
APPLICANT: ZAMB, TIM
APPLICANT: ZAMB, TIM
APPLICANT: TIZPATRICK, DAVID
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1
TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOREISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 4; Length 420;
Pred. No. 72;
0; Mismatches 2; Indels
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COUNTRY: USA

ZIP: 94304-1018

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERAING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

RELING DATE: 12-7UL-1996

CLASSIFICATION: 536

ATTORNEY AGENT INFORMATION:

RAGISTRATION NUMBER: 35,636

REFERENCE/DOCKET NUMBER: 29310-20005.10

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08682847 Patent No. 5858989 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEQ 1D NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.4%;
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LENGTH: 521 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.0

- 1, Conservative
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Job time : 14.6729 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

6, 2004, 15:52:34; Search time 10.0935 Seconds (without alignments) 85.771 Million cell updates/sec

US-10-009-709-8 56 1 GHPRPPRGR 9 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_78:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	escription	salivary proline-r	livary proline	roline-rich			ய	alpha-2B-adrenergi	drenerg	alpha-2-C2 adrener		CL1AA protein - ra	hilin-1. b	٠,	latrophilin-1, bra	. 1	CL1BB protein - ra	hõinositide	fatty-acid synthas	hypothetical prote			10)Ľ	u	of	vlat	t)	rythrocyte	ומי
SUMMARIES	Д	HUS	B25372	730	_4	0	65	151883	64	22	A46419	T17138	T18411	T17149	T18413	T17145	T17156	E59431	JC4743	500945	F71241	F91020	AC0398	33	A91061	G85905		297	74	977
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	Score		99		44	43	43	42		42	41	41	41	41	41	41	41	41	41					40	40	40	40	40	40	
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hypothetical prote	hypothetical prote	Ω	qene alx3 protein	hypothetical prote	heterogeneous nucl	delta-(L-alpha-ami	elkl protein - mou	nitrilotriacetate	calcium channel pr	hypothetical prote	PTB-associated spl	C-arrestin - rat (al	hypothetical prote	312.9
H82546	255609	AC0629	148185	C70641	T02673	S18268	JC4965	AB3238	A37860	T20566	A46302	170113	A72701	D72579	A88637
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151	200	226	346	470	633	3649	429	450	1852	2911	707	92	107	123	137
9.69	9.69	9.69	9.69	9.69	9.69	9.69	67.9	67.9	67.9	67.9	67.0	66.1	66.1	66.1	66.1
	39	39	39	39	9	9	38	38	38	38	37.5	37	37	37	37
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

AL I GNMENTS

RESULT 1 Paltyzer Paltyzer Paltyzer Paltyzer N;Alternate names: salivary acidic proline-rich protein PRH2 N;Alternate names: salivary acidic proline-rich protein PRH2 N;Contains: peptide PC (basic proline-rich peptide IB-8b); proline-rich phosphoprotei C;Species: Homo sapiens (man) C;Date: 31-Mar-1981 #sequence_revision 12-Apr-1996 #text_change 08-Dec-2000
C;Accession: A25372; A19803; B57868; A92277; A92254; A94425; A91954; S02564; S02563; J F;Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O. J. Biol. Chem. 260, 11123-11130, 1985
A,Title: Differential RNA splicing and post-translational cleavages in the human saliv A;Reference number: A92492; MUID:85289325; PMID:2993301 A;Accession: A25372

Ny Molecule type: mRNA Ny Residues: 1-166 kMAE> Ny Residues: 1-166 kMAE> Ny Cross-references: GST (8703202; NID:g190481; PIDN:AAAG0183.1; PID:g190482 Ny Schlesinger, D.H.; Hay, D.I. Ny Schlesinger, D.H.; Hay, D.I. All Title: Primary structure of the active tryptic fragments of human and monkey salivar Ny Reference number: A91757; MUID:81191179; PMID:7228490

Accession: A19803

Wolecule type: protein
',Rolecule type: protein
',Readdues: 17.46 < SCH>
',Kim, H.S.; Maeda, N.
', Biol. Chem. 261, 6712-6718, 1986
',Title: Structures of two HaeIII-type genes in the human salivary proline-rich protei

Molecule type: DNA

);Residues: 1.166 <KIM>
A;Cross-references: GB:M13056; NID:g190513; PIDN:AAA98808.1; PID:g190514
S;Wong, R.S.C.; Bennick, A.
J. Bhol, Chem. 255, 5943.5948; 1980
A;Title: The primary structure of a salivary calcium-binding proline-rich phosphoprote sylchence number: A92277; MUID:80204368; PMID:7380845

A;Accession: A92277
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 17-19, 'W',21-166 <WGN>
A;Residues: 17-19, 'W',21-166 <WGN>
A;Note: the amino-terminal 46 residues are involved with inhibiting hydroxyapatite for R;Mongy R.S.C.'; Hofmann, T.; Bennick, A.
J. Biol. Chem. 254, 4800-4808, 1979
A;Title: The complete primary structure of a proline-rich phosphoprotein from human sa A;Reference number: A92254; MUID:79173237; PMID:438215
A;Accession: A22264

A;Molecule type: protein A;Residues: 17-19,'N',21-122 <WO2> R;Schlesinger, D.H.; Hay, D.I. Peptides: Structure and Biological Function (Proc. Sixth Amer. Peptide Symp.), Gros A;Title: Complete primary structure of a proline-rich phosphoprotein (PRP-4), a potent A;Reference number: A94425

Molecule type: protein Residues: 17-166 <HAY> Accession: S02563

Accession: JP0106

Accession: S06153

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salivary proline-rich phosphoprotein precursor PRH1 (allele PIF) - human C,Species: Homo sapiens (man) C,Species: Homo sapiens (man) C,Species: S2-Aug-1987 #text_change 20-Aug-1999 C,Accession: B25372; A57868; S02862; G38355; S06153; B27307 R,Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O. M. S. Azen, E.A.; Smithies, O. M. J. Kim, H.S.; Azen, B.A.; Smithies, O. A;Title: Differential RNA splicing and post-translational cleavages in the human saliv, A;Reference number: A92492; MUD:85289325; PMID:2993301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecule type: DNA
1,Residues: 1-166 <KIM>
1,Cross-references: GS-M13057; NID:g190511; PIDN:AAA98807.1; PID:g190512
1,Cross-references: GS-M13057; NID:g190511; Minaguchi, K.; Madapallimattam, G.; Schlusiochem. J. 255, 15-21, 1988
1,Crochem. J. 255, 15-21, 1988
1,Crochem. J. 255, 15-21, 1988
1,Title: The primary structures of six human salivary acidic proline-rich proteins (PR)
1,Reference number: S02562; MUID:89061650; PMID:3196309
                                                                                                                                                                                                                                                                                                                                                                                                                     A)Residues: 1-166 <MAE>
A)Cross-references: GB:X03203; NID:g190483; PIDN:AAA60184.1; PID:g190484
A)Cross-references: GB:X03203; NID:g190483; PIDN:AAA60184.1; PID:g190484
B; Kim, H. S.; Maeda, N.
J. Biol. Chem. 261, 6712-6718, 1986
A)Title: Structures of two HaeIII-type genes in the human salivary proline-rich protei: A,Reference number: A57868; MUID:86196106; PMID:3009472
A,Accession: A57869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: protein
Residues: 123-166 <KAU>
Robinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
lochem. J. 263, 497-503, 198
Horinem. J. 263, 497-503, 198
Horiner, Brimary structure and possible origin of the non-glycosylated basic proline-r
Reference number: S06153; MUID:90088384; PMID:2688632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: protein
A,Residues: 123-166 eROB>
R.A.Zen, B.A., Kim, H.S., Goodman, P.; Flynn, S.; Maeda, N.
Am. J. Hum. Genet. 41, 1035-1047, 1997
A;Attle: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich
A;Reference number: A27307; MUID:88074309; PMID:3687941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Molecule type: protein
;Residues: 47-71 <HAY>
;Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
jochemistry 30, 3351-3356, 1991
;Title: Basic proline-rich proteins from human parotid saliva: relationships of
;Reference number: A38355; MUID:91190884; PMID:1849422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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N;Alternate names: salivary acidic proline-rich protein
C;Species: Homo sapiens (man)
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A;Map position: 12p13.2-12p13.2
A;Introns: 22/1, 34/1
C;Superfamily: proline-rich protein
C;Superfamily: proline-rich protein
C;Keywords: phosphoprotein; saliva; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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A,Molecule type: DNA
A,Residues: 17-41, L', 43-118,'C',120-166 <AZE>
A,Cross_references: EMBL:K03203
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Conservative 0
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nes 9; Conserv
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Matches
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C; Superfamily: proline-rich protein
C; Superfamily: proline-rich protein
C; Superfamily: proline-rich protein
C; Superfamily: proline-rich protein
C; Superfamily: proline-rich prosphogrotein; pyroglutamic acid; saliva
E; 1-16/Domain: signal sequence #status experimental <PRC>
F; 17-16/Product: protein C #status experimental <PRC>
F; 17-12/Product: protein A #status experimental <PRA>
F; 17-46/Product: protein A #status experimental <PRP>
F; 17-46/Product: PRP: 3 #status experimental <PRP>
F; 17-16/Product: PRP: 3 #status experimental <PRP>
F; 17-16/Product: poptide P-C #status experimental <PRC>
F; 17-16/Product: poptide (Ger) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 123-166 <1SE>
R;Hay, D.I.; Bennick, A.; Schlesinger, D.H.; Minaguchi, K.; Madapallimattam, G.; Schluck
Biochem. J. 255, 15-21, 1988
A;Title: The primary structures of six human salivary acidic proline-rich proteins (PRP-A;Reference number: S02562; MUID:89061650; PMID:3196309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: protein
.Residues: 47-71 <HA2>
.Schlesinger, D.H.; Hay, D.I.
.Tit. J. Pept. Protein Res. 27, 373-379, 1986
.Title: Complete covalent structure of a proline-rich phosphoprotein, PRP-2, an inhibit Reference number: JP0106, MUID:86222916; PMID:3710693
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Molecule type: protein
Molecule type: protein
Robinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
Robinson, T.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
Robinson, T. 263, 497-503, 1989
Filtle: Primary structure and possible origin of the non-glycosylated basic proline-rid
Reference number: S06153; MUID:90088384; FMID:2688632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: protein
Residues: 17-161, Q', 163-166 <8C3>
Experimental source: parotid gland
Radifman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
iochemistry 30, 3354-3356, 1991
1141e: Basic proline-rich proteins from human parotid saliva: relationships of the cov
Reference number: A38355; MUID:91190884; PMID:1849422
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                                                                                                                                                                                                                                                     A,Title: The amino acid sequence of a salivary proline-rich peptide, P-C, and its relati
A,Reference number: A91954; WUID:80227634; PMID:7390979
A;Contents: peptide P-C
A,Accession: A91954
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Residues: 123-166 <ROB>
;Comment: The proposed biological functions are a highly potent inhibitor of crystal
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100.0%; Pred. No. 0.11;
iive 0; Mismatches
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A;Map position: 12p13.2-12p13.2
A;Introns: 22/1; 34/1
                                                                                A;Molecule type: protein
A;Residues: 17-122 <SC2>
A;Note: the authors call this protein PRP-4
K:Isemura, S.; Saitoh, E.; Sanada, K.
J. Biochem. 87, 1071-1077, 1980
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Ouery Match Best Local Similarity 100.

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RESULT 2 B25372

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Gaps

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Cispecies: Aeropyrum pernix.
Cipate: 20-Aug-1999 #text_change 28-Jul-2000
Cipate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000
Cipate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000
Cipates 28-Jul-2000
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawarabayasi, Y.; Hino, Y.; Tamawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
A;Til-a: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72654
A;Accession: B72654
A;Accession: B72654
A;Accession: Preliminary
A;Molesule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cipecies: Rattus norvegious fau:
Cipecies: Rattus norvegious (Norway rat)
Cipace: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
Cipace: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
Ride Josseo, M.; Cloix, J.F.; Pecquery, R.; Giudicelli, Y.; Dausse, J.F.
Am. J. Hypertens 8, 177-182, 1995
Antitle: Differential sodium regulation between salt-sensitive and salt-resistant Sabr. A.Reference number: 151883; MUID:95275492; PMID:7755946
A.Reference number: 151883; MUID:95275492; PMID:7755946
A.Residus: preliminary; translated from GB/EMBL/DDBJ
A.Residus: 1-448 cRBS>
A.Residus: 1-448 cRBS>
A.Residus: 1-448 cRBS>
A.Constantially: vertebrate rhodopsin
C; Ruperfamily: vertebrate rhodopsin
C; Ruperfamily: vertebrate rhodopsin
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A; Residues: 1.438 <KAW>
A; Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79634.1; PID:95104319
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C.Species: Rattus norvegicus (Norway rat)
C.Jate: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C.Accession: A35642
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    Aeropyrum pernix (strain K1)

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C;Superfamily: histidine-tRNA ligase; histidine-tRNA ligase homology
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                                                                  DB 2; Length 340;
20;
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                                                              Score 43; DB
Pred. No. 20;
0; Mismatches
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Pred. No. 25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       probable histidyl-tRNA synthetase APE0662
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                                                           Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 87.5%;
Matches 7; Conservative
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C,Genetics:
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                                                                                                                                                                                                                                                           330 GRPRPPRG 337
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C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_cnange 27-nug-1227,
C;Accession: A27307
R;Azen, E.A.; Kim, H.S.; Goodman, P.; Flynn, S.; Maeda, N.
Am. J. Hum. Genet. 41, 1035-1047, 1987
A;Title: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich pro
A;Reference number: A27307; MUID:88074309; PMID:3687941
A;Accession: A27307
A;Accession: A27307
A;Residues: nucleic acid sequence not shown
A;Molecule type: DMA
A;Molecule type: DMA
A;Residues: 1-17 cAZE>
A;Cross-references: EMBL:K03203
C;Genet: GDB:PRH1
A;Cross-references: GDB:119515; OMIM:168730
C;Genet: GDB:PRH1
A;Cross-references: CDB:119515; OMIM:168730
C;Superfamily: proline-rich protein
C;Keywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Rv1215c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: E70610
C;Accession: E70610
R;Cole, S.T., Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S;Cohnor, R.; Davies, R.; Devihin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Recerence number: A70500; MUID:98295987; PMID:9634230
A;Status: preliminary, nucleic acid sequence not shown; translation not shown
B; Besidues 1551
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A;Residues: 1-561 <COL>
A;Cross-references: GB:293777; GB:AL123456; NID:g3261726; PIDN:CAB07817.1; PID:e311160; A;Experimental source: strain H37Rv C;Genetics: A;Gene: Rv1215c
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C; Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 18-Jun-1999
C; Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 18-Jun-1999
C; Accession: A24026
B; Roberts, A.N.; Hudson, G.S.; Brenner, S.
Gene 35, 259-270, 1985
A; Reference number: A24026
A; MUD: 86006275; PMID: 4043733
A; Residues: 1340 < ROB>
A; Roberts in 340 < ROB>
A; Roberts in 340 < ROB>
C; Superfamily: FRNA (adenine-N6-)-methyltransferase
C; Superfamily: RNA (adenine-N6-)-methyltransferase
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100.0%; Score 56; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels
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Pred. No. 23;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erythromycin resistance protein - Arthrobacter sp.
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Best Local Similarity 87.5%;
Matches 7; Conservative 1
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534 YPRPPRGR 541
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Gaps

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Date: 15-Oct-117138
C;Accession: T17138
R;Krasnopercv, V.G.; Bittner, M.A.; Beavis, R.; Kuang, Y.; Salnikow, K.V.; Chepurny, O Neuron 18, 25-937, 1997
A;Title: Alpha-Latroctoxin stimulates exocytosis by the interaction with a neuronal G-p: A;Accession: T17138
A,Title: Cloning and sequencing of a trophoblast-endothelial-activated lymphocyte surf; A,Reference number: A46419; MUID:93066251; PMID:1438229 A,Accession: A46419
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FBBS Lett. 443, 348-352, 1999
A;Ttle: The latrophilin family: multiply spliced G protein-coupled receptors with dif A;Reference number: Z18869; MID:99148828; PMID:10025961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-1466 < kRA> A; Cross-references: EMBL: AF081144; NID: 93695114; PID: 93695115; PIDN: AAC62650.1 C; Superfamily: alpha-latrotoxin receptor, calcium-independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-1467 <MAT>
A; Cross-references: EMBL: AF111097; NID: 94185801; PID: 94185802; PIDN: AAD09191.1
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N;Alternate names: alpha-latrotoxin receptor, calcium-independent
C;Species: Bos primigenius taurus (cattle)
C;Date: i5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                           A; Residues: 1-550 «VOL»
A; Residues: 1-550 «VOL»
A; Residues: 1-550 «VOL»
A; Cross-references: GB: M99578; NID: 9187241; PIDN: AAA36187.1; PID: 9187242
A; Cross-reference in Carracted from NCBI backbone (NCBIN: 117872; NCBIP: 117873)
A; Note: sequence extracted from NCBI backbone (NCBIN: 117872; NCBIP: 117873)
B; Rillison, J.W.; Ramos, C.; Yen, P.H.; Shapiro, L.J.
Hum. Mol. Genet. 1, 691-696, 1992
A; Title: Structure and expression of the human pseudoautosomal gene XE7.
A; Reference number: 154325; MUID: 93258310; PMID: 1302606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: 168598
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-384, L', «RES>
A;Cross-references: GB:L03426; NID:g340386; PIDN:AAA61303.1; PID:g340387
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77.8%; Pred. No. 1.6e+02;
tive 0; Mismatches 2; Indels
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 64;
0; Mismatches
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 77.0
7; Conservative
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A;Introns: 254/3; 304/2; 384/3
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                                                                                                                               A;Status: preliminary
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A; Status: preliminary
A; Molecule type: DNA
B; Cother the authors translated the codon CCA for residue 161 as Phe, ACT for residue 337
A; Note: the authors translated the codon CCA for residue 161 as Phe, ACT for residue 337
A; Molecule type: DNA
A; Recession: JH0693; MUD: 92378586; PMD: 1354956
A; Accession: JH0693; MUD: 92378586; PMD: 1354956
A; Accession: JH0693
A; Molecule type: DNA
A; Residues: 6-228, 231-455
A; Cross-references: GB: L00979; NID: 9191847; PIDN: AAA37131.1; PID: 9191548
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane predicted <TM2>
F; 55-81/Domain: transmembrane #status predicted <TM3>
F; 173-199/Domain: transmembrane #status predicted <TM3>
F; 173-199/Domain: transmembrane #status predicted <TM5>
F; 174-199/Domain: transmembrane #status predicted <TM5>
F; 174-02/Domain: transmembrane #status predicted <TM5>
F; 174-0435/Domain: transmembrane #status predicted <TM7>
F; 174-0435/Domain: transmembrane #s
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A;Title: Molecular characterization of a rat alpha-2B-adrenergic receptor. A;Reference number: A35642; MUID:9022177; PMID:2158103
A;Molecule type: mRNA
A;Residues: 1-453 < ZENN
A;Cross-references: GB:M32061; NID:g202589; PIDN:AAA40635.1; PID:g202590
A;Cross-references: GB:M2061; NID:g202589; PIDN:AAA40635.1; PID:g202590
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
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C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46419; 16859
R;Voland, J.R.; Wyzykowski, R.J.; Huang, M.; Dutton, R.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 10425-10429, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-2-C2 adrenergic receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
C;Accession: S28221; JH0693
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85.7%; Pred. No. 37;
Eive 1; Mismatches 0; Indels
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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C;Superfamily: alpha-latrotoxin receptor, calcium-independent C;Keywords: G protein-coupled receptor

1258 GAPEPPŔĠŔ 1266

CLIBA protein - rat

1 GHPRPPRGR 9

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Accession: T1745

R.Sugatta, S.; Ichtchenko, K.; Khvotchev, M.; Sudhof, T.C.

R.Sugatta, S.; Ichtchenko, K.; Khvotchev, M.; Sudhof, T.C.

R.Sugatta, S.; Ichtchenko, K.; Khvotchev, M.; Sudhof, T.C.

A.Reference number: 218712

A.Recession: T1745

A.Recession: T1745

A.Recession: T1745

A.Residues: 1-1510 < SUG>

A.Residues: 1-1510 < SUG>

A.Cross-references: EMBL:AF081145; NID:g3695117; PIDN:AAC62651.1

C.Superfamily: alpha-latrotoxin receptor, calcium-independent
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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A;Molecule type: mRNA
A;Residues: 1471 <SUGA
A;Residues: 1471 <SUGA
A;Coss-references: EMBL:AF081146; NID:g3695118; PID:g3695119; PIDN:AAC62652.1
C;Superfamily: alpha-latrotoxin receptor, calcium-independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Accession: T17149
Rsquence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T17149
R;Sugita, S; Ichtchenko, K.; Khvotchev, M.; Sudhof, T.C.
submitted to the EMBL Data Library, July 1998
A;Bescription: CL family.
A;Reference number: Z18712
A;Accession: T17149
                                                                                                                                                                   Gaps
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                                                                            Query Match 73.2%; Score 41; DB 2; Length 1467; Best Local Similarity 77.8%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 2; Indels
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C;Accession: T18413
R;Matsushita, H.; Lelianova, V.G.; Ushkaryov, Y.A.
FEBS Lett. 43, 348-352, 1999
A;Title The latrophilin family: multiply spliced G protein-coupled receptors with diffe A;Feference number: Z18869; MUID:99148828; PMID:10025961

Alternate names: alpha-latrotoxin receptor, calcium-independent;Species: Bos primigenius taurus (cattle);Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

latrophilin-1, brain-specific - bovine

1263 GGPEPPRGR 1271

1 GHPRPPRGR 9

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A;Molecule_type: mRNA A;Residues: 1-1472 <MAT> A;Cross-references: EMBL:AF111098; NID:g4185803; PID:g4185804; PIDN:AAD09192.1 A;Experimental source: brain

A;Status: preliminary; translated from GB/EMBL/DDBJ

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Gaps

Query Match 73.2%; Score 41; DB 2; Length 1472; Best Local Similarity 77.8%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 2; Indels

T17145 CLIAB protein - rat C;Species: Rattus norvegicus (Norway rat)

RESULT 15

1263 GAPEPPRGR 1271

1 GHPRPPRGR 9

A,Gene: LPH1 C,Superfamily: alpha-latrotoxin receptor, calcium-independent C,Keywords: G protein-coupled receptor

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Gaps

Query Match 73.2%; Score 41; DB 2; Length 1471; Best Local Similarity 77.8%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 2; Indels

Tue Apr

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NCBI_TaxID=9606;
                                                                                                                                 HUMAN
                                                                                                                                PRPC HUN
P02810;
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PRPC HUMAN
                                                                                                                                 909891 arthrobacte
09yeb2 aeropyrum p
P1928 rattus norv
P193645 mus musculu
08x9f0 escherichia
08fez9 escherichia
91747 haemophilus
08x9g2 salmonella
08zyy7 yersinia pe
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                                        April 6, 2004, 15:31:19; Search time 5.80374 Seconds (without alignments) 80.746 Million cell updates/sec
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Q8tpx0
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Q9wu83
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P02812
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                         141681 segs, 52070155 residues
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RLUD_SALIY
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LENG WOUSE
LLENG RAI
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Maximum Match 100%
Listing first 45 summaries
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ERMA_ARTS3
SYH ÄERPE
A2AB RAT
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RLUD_ECOL6
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METAC
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PRP2_HUMAN
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                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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	P04280 homo sapien	P03345 human t-cel	P14076 human t-cel	P14077 human t-cel		Q9fg77 arabidopsis		P21519 drosophila				P30796 pracmys nat		
	PRP1 HUMAN	GAG HILLA	GAG_HTL1C	GAG_HTL1M	VGLC HSVBC	WRK2_ARATH	YMS5 CAEEL	MAM DROME	TABP HUMAN	CYT2_ORYSA	GASR HUMAN	GASR_PRANA		ALIGNMENTS
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!	37	37	37	37	37	37	37	37	37	36	36	36		
	34	35	36	37	38	39	40	41	42	43	44	45		

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PERSULT 1

PERCHAMAN STANDARD; PRT; 166 AA.

TO 1-MAR-1999 (Rel. 0), Created)

TO 1-MAR-2004 (Rel. 4), Last annotation update)

TO 1-MAR-2004 (Rel. 4), Last annotation update)

DT 15-MAR-2004 (Rel. 4), Last annotation update)

Equipment and the property acidic proline-rich phosphoprotein 1/2 precursor (RRP-1/PRP-1) (Rel. 4), Last annotation update)

DE 15-MAR-2004 (Rel. 4), Last annotation update)

Equipment and the property acidic proline-rich phosphoprotein 1/2 precursor (RRP-1/PRP-1) (RRP-1/PRP-1/PRP-1) (RRP-1/PRP-1) (RRP-1/PR-1) (RRP-
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SALIVARY ACIDIC PROLINE-RICH

166

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SEQUENCE OF 17-46
MEDLINE=81191179;
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1 GHPRPPRGR
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                                                                                                                   123
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P09891;
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A frequent mutation in the acidic proline-rich protein gene, PRH2, causing a 0147K change closely adjacent to the bacterial binding domain of the cognate salivary PRP (Prl') in Afro-Americans."; Hum. Mutat. 12:72-72(1998).
-!- PUNCTION: PRP's act as highly potent inhibitors of crystal growth of calcium phosphates. They provide a protective and reparative environment for dental enamel which is important for the integrity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 17-122 (PROTEIN A).
Schlesinger D.H., Hay D.I.;
"Complete primary structure of a proline-rich phosphoprotein (PRP-4), a potent inhibitor of calcium phosphate precipitation in human parotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLUIAR LOCATION: Secreted.

PTM: Proteolytically cleaved; PRP-2, PRP-1, and PIF-S yield PRP-4, PRP-3 (protein A), and PIF-F, respectively.

POLYMORPHISM: Allele PRH1-4 is also known as PRH DA allele; allele PRH2-1 is also known as PRH or protein C; allele PRH2-3 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 123-166 (PEPTIDE P-C).
MEDLINE-80227634; PubMed=7390979;
ISSEMURA S., Saltch E., Sanada K.;
"The amino acid sequence of a salivary proline-rich peptide, P-C, and its relation to a salivary proline-rich phosphoprotein, protein C.";
J. Biochem. 87:1071-1077 (1980).
                                                                                                                                                                                                                                                                                                                             MEDLINE=79173237; PubMed=438215;
Wong R.S.C., Hofmann T., Bennick A.;
"The complete primary structure of a proline-rich phosphoprotein from
human saliva.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           July Gross E., Meienhofer J. (eds.);
Peptides: structure and biological function (Proceedings of the 6th American peptide symposium), pp.133-136, Pierce Chemical Co.,
"The primary structure of a salivary calcium-binding proline-rich phosphoprotein (protein C), a possible precursor of a related salivary protein A.";
J. Biol. Chem. 255:5943-5948(1980).
                                                                                                                                                                          Schlesinger D.H., Hay D.I.;
"Primary structure of the active tryptic fragments of human and monkey salivary anionic proline-rich proteins.";
int. J. Pept. Protein Res. 17:34-41(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM, 168710; -.
GO; GO:0005615; C:extracellular space; TAS.
Repeat; Parctid gland; Phosphorylation; Signal; Polymorphism;
Pyrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 254:4800-4808(1979).
                                                                                                                                                     PubMed=7228490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K03202; AAA60183.1; --
EMBL; K03203; AAA60184.1; --
EMBL; M13057; AAA98807.1; --
EMBL; M13058; AAA98808.1; --
Genew; HGNC:9366; PFH1.
Genew; HGNC:9367; PRH2.
MIM; 168730; --
MIM; 168790; --
                                                                                                                                                                                                                                                                                                        SEQUENCE OF 17-122 (PROTEIN A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT PRH2-3 LYS-163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the teeth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE-80006275; PubMed-4043733;
Roberts A.N., Hudson G.S., Brenner S.;
"An erythromycin-resistance gene from an erythromycin-producing strain of Arthrobacter sp.";
Gene 35:259-270(1995)
-!- FUNCTION: THIS PROTEIN PRODUCES A DIMETHYLATION OF THE ADENINE RESIDED AT POSITION 2058 IN 238 RRNA, RESULTING IN REDUCED AFFINITY BETWEEN RIBOSOMES & MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN E
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                  HYDROXYAPATITE FORMATION, BIND
                                                                                                                                                                                                                                                                                                                                                   ..
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01-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
11-mosamide-streptogramin B resistance protein) (Brythromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arthrobacter sp. (strain B3381).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Propionibacterineae, Nocardioidaceae, Aeromicrobium.
                                                                                                                                                                                                                                                                                                                100.0%; Score 56; DB 1; Length 166; 100.0%; Pred. No. 0.041;
                                                                                       CALCIUM.
PHOSPHOPROTEIN 1/2.
SALIVARY ACIDIC PROLINE-RICH
                                                                                   TO HYDROXYAPATITE AND CALCIU PYRROLIDONE CARBOXYLIC ACID. PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                      D -> N (in allele PRH1-4).

/FTId=VAR 005563.

D -> N (in allele PRH2-1).

/FTId=VAR 005564.

Q -> K (in allele PRH2-3).
                                                                                                                                                                                                                                           /FTId=VAR 005565.
F -> P (IN REF. 10).
A7DF62BF94E3C3EF CRC64;
                                   PHOSPHOPROTEIN 3/4.
                                                                                                                                           PHOSPHORYLATION
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                                                    PEPTIDE I
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InterPro; IPR001737; RRNA A dimeth.
InterPro; IPR000051; SAM Dind.
Pfam; PF00398; RrnaAD; 1.
SMART; SM00650; rADC; 1.
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Matches 9; Conserv
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us-10-009-709-8.rsp

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                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; 872654; 872654; B. 1020...
HANAP; MR 00127; -1.
HANAP; MF 00127; -1.
InterPro; IPR004516; HisS.
InterPro; IPR004516; HisS.
InterPro; IPR00219; HGTP_anticodon.
InterPro; IPR00519; HGTP_anticodon; 1.
Pfam; PF03129; HGTP_anticodon; 1.
Pfam; PF03129; HGTP_anticodon; 1.
TIGRPAMS; TIGR00442; hisS; 1.
PROSTIE; PS50862; AA TRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                         Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                          76.8%; Score 43; DB 1; Length 340;
87.5%; Pred. No. 8.7;
ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.8%; Score 43; DB 1; Length 438; 87.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
PROSITE; PS01131; RRNA_A DIMETH; 1.
Antibiotic resistance; Transferase.
SEQUENCE 340 AA; 37453 MW; E99A714C391952B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 AA; 49111 MW; ECCE67F59A9FB7BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  438 AA
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NCBI_TaxID=56636;
                                                                                 Query Match
Best Local Similarity 87.57
7; Conservative
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SEQUENCE 438 AA
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Q9YEB2;
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SYH_AERPE
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Gaps

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1; Indels

0; Mismatches

Best_Local Similarity 87.5: Matches 7; Conservative

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proteins.
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zeng D., Harrison J.K., D'Angelo D.D., Barber C.M., Tucker A.L., Lyndh K.R.; "Dyndh K.R." Hoblecular characterization of a rat alpha 2B-adrenergic receptor."; Proc. Natl. Acad. Sci. U.S.A. 87:3102-3106(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Sprague-Dawley;
Schaak S., Cussac D., Paris H.;
"Cloning and characterization of the rat alpha2B-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors mediate the catecholamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am. J. Hypertens. 8:177-182(1995).
-1- FUNCTION: Alpha-2 adrenergic receptors mediate the catecholamine
induced inhibition of adenylate cyclase through the action of G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       le Jossec M., Cloix J.F., Pecquery R., Giudicelli Y., Dausse J.P., "Differential sodium Jegulation between salt-sensitive and salt-resistant Sabra rats is not due to any mutation in the renal alpha 2B-adrenoceptor gene.";
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DR PRINTS; PRO0037; GPCR.RHODDPSN.
DR PROSITE; PSO3625; GPROTEIN RECEP_F1_1; 1.

DR PROSITE; PSO3625; GPROTEIN RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Multigene family; KW Phosphorylation; Lipoprotein; Paintate.

FT G-protein Coupled receptor; Transmembrane; Multigene family; Transmembrane; Multigene family; Transmembrane; Multigene family; Transmembrane; Multigene family; Transmembrane; Transm
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                                                                                                                                                                                                                                                                                 P19326; Q63021, Q925E4; Orested)
01-NOV-1990 (Rel. 16, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
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MEDLINE-95275492; PubMed-7755946;
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MEDLINE=90222177; PubMed=2158103;
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EMBL; AF366899; AAK53388.1; -
EMBL; X74400; CAA52411.1; -.
PIR; A35642; A35642.
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7 GRPRPPRG 14
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EMBL; M94583; AAA73895.1; -.
EMBL; L00979; AAA37131.1; ALT_INIT.
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                                            PIR, S28221, S28221.
HSSP, P29274, 1MMH.
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455 AA;
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Best Local Similarity
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RLUD_ECO57
ID RLUD E
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92378586; PubMed=1354956; Chruscinski A.J., Link R.E., Daunt D.A., Barsh G.S., Kobilka B.K.; Chruscinski A.J., Link R.E., Daunt D.A., Barsh G.S., Kobilka B.K.; adrenergic receptor."; Biochiem. Biochem. 
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                            IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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STRAIN-DBA/2; TISSUE=Liver;
MEDLINE=93129625; Pubmde=1336396;
Chen W.-M., Chang A.C., Shie B.J., Chang Y.-H., Chang N.-C.A.;
"Molecular cloning and characterization of a mouse alpha 2C2
                                                                                                                                                                 S-palmitoyl cysteine (Potential). ASP/GLU-RICH (ACIDIC). IMPLICATED IN LIGAND BINDING (BY
                                                                                                                                                                                                                                                                                                                                                    75.0%; Score 42; DB 1; Length 453; 85.7%; Pred. No. 17; 1.1ve 1; Mismatches 0; Indels
                                            EXTRACELLULAR (POTENTIAL).
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CBA69CE23EACB511 CRC64;
                                                            5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
              (POTENTIAL).
                                                                                                                                    CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CTT-2003 (Rel. 42, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
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3 (POTENTIAL)
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Biochim. Biophys. Acta 1171:219-223(1992)
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                                                                                                                                                                                                                                                                                                                        50369 MW;
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254 GHPKPPR 260
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162 1
453 AA;
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 185
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Gaps
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IMPLICATED IN CATECHOL AGONIST BINDING
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IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).
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10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)
Ribosomal large synthase) (Uracil hydrolyase).
Ribo or SFHB OR 23888 OR ECS3457.
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteria; Enterobacteria; Cammaproteobacteria; Cammaproteobacteria;
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STRAIN=0157:#7 / EDL933 / ATCC 700927;
MEDLINE=12074935; PubMed=11206551;
Perrai N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
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ASP/GLU-RICH (ACIDIC)
IMPLICATED IN LIGAND BINDING (BY
GO, GO:0004938; F:alpha2-adrenergic receptor activity; IDA.
GO; GO:0001525; P:anglogenesis; IMP.
GO; GO:000155; P:maglogenesis; IMP.
GO; GO:000165; P:MapKKK cascade; IMP.
InterPro; IPR000275; GPCR Rhodpsn.
PRINTS; PR000237; GPCR Rhodpsn.
PROSITE; P800237; G RROTEIN RECEP F1 1; 1.
PROSITE; P800237; G RROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Transmembrane; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
DOMAIN.

EXTRACELLULAR (POTENTIAL).
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Pred. No. 17;
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
5 (POTENTIAL).
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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MISSING (IN REF. 2).
A3954AD76E0E6263 CRC64;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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1; Mismatches
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                                                                                                                                                Gaps
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Appdaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., "Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.", Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                         5'-phosphare + H(2)0.
-!- SIMILARITY: Belongs to the pseudouridine synthase rlua family.
-!- SIMILARITY: Contains 1 S4 RNA-binding domain.
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QBFEZ9; QB3Q10;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)
(Pseudouridylate synthase) (Uracil hydrolyase).

Escherichia coli O6, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.4%; Score 40; DB 1; Length 325; 75.0%; Pred. No. 24; tive 1; Mismatches 1; Indels
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DOMAIN 17 90 SA RNA-BINDING.
ACT. SITE 136 138 BY SIMILARITY.
SEQUENCE 325 AA; 36990 MW; 78046623A4558967 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IRR006225; Pseud synth Rlub.
InterPro; IRR006145; PseudoU synth.
InterPro; IPR00624; Rlu_synth.
InterPro; IPR002942; S4.
Pfam; PR00849; PseudoU_synth_2; 1.
Pfam; PF01479; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO005; rluD subfam; 1.
PROSITE; PS01129; PS1 RLU; 1.
PROSITE; PS50889; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE005490; AAG57707.1; -. EMBL; AP002562; BAB3680.1; -. PIR; A91061; A91061.
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                                                                                                                                     SEQUENCE FROM N.A
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OR Bacterial, Pacchebacterial, Gammagrotechaateria, Enterobacteriales;

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MEDLINE=20537953; PubMed=11087118;
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MUTAGEN
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RLUD HAEDU
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MEDLINE=99029898; PubMed=9814761;
Raychaudhuri S., Conrad J., Hall B.G., Ofengand J.;
"A pseudouridine synthase required for the formation of two
universally conserved pseudouridines in ribosomal RNA is essential for normal growth of Escherichia coll.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K., Itch T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Oshinoto H., Oshama S., Saito N., Sampei G., Saroh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuchi T., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuchi T., Toonetruction of a contiguous 874-kb sequence of the Escherichia coli -- KI2 genome corresponding to 50.0-68.8 min on the linkage map and DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91294165; PubMed=1906060;
Kitegawa M., wada C., Yoshioka S., Yura T.;
"Expression of ClpB, an analog of the Arp-dependent protease
regulatory subunit in Escherichia coli, is controlled by a heat shock
                                                                    Gaps
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STRAIN=KIZ / MG1655,
MEDGINE PROM N.A.
STRAIN=KIZ / MG1655,
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III., Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mub B., Shao Y.,
"The Complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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P33643; P77003;
01-F2B-1994 (Rel. 28, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
110-CCT-2003 (Rel. 42, Last annotation update)
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)
(Pseudouridylate synthase) (Uracil hydrolyase).
RLUD OR SFHB OR B2594.
                   Score 40; DB 1; Length 325;
Pred. No. 24;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogura T., Tomoyasu T.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97349980; PubMed=9205837;
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Bacteriol. 173:4247-4253(1991)
                          71.4%;
75.0%;
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Ouery Match
Best Local Similarity 75...
6, Conservative
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                                                                                                                                                             254 GRPRPPKG 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                              MEDLINE=21345619; PubMed=11453071; Gutgsell N.S., Del Campo M., Raychaudhuri S., Ofengand J.; Gutgsell N.S., Del Campo M., Raychaudhuri S., Ofengand J.; A second function for pseudouridine synthases: A point mutant of Rlub unable to form pseudouridines 1911, 1915, and 1917 in Escherichia coli 23S ribosomal RNA restores normal growth to an Rlub-minus strain."; RNA 7:990-998 (2001)
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EKEPPROALATATMLENTHPISCIBENHAPIDEDDNVELLEV

MRADPEEHKDEVDWL -> ACVSLTARRYMOPCCVFITRSP

ASKWNGWRLPHKIWWS (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at positions 1911, 1915 and 1917 in 238 ribosomal RNA.

-!- FUNCTION: Responsible for synthesis of pseudouridine from uracil
at positions 1911, 1915 and 1917 in 238 ribosomal RNA.

-!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
5'-phosphate + H(2)0.

-!- SIMILARITY: Belongs to the pseudouridine synthase rluA family.

-!- SIMILARITY: Contains 1 S4 RNA-binding domain.

-!- CAUTION: Ref. 4 sequence differs from that shown due to a frameshift in position 133.
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Wrzesinski J., Bakin A., Ofengand J., Lane B.G.; "Isolation and properties of Escherichia coli 23S-RNA pseudouridine 1911, 1915, 1917 synthase (RluD)."; IUBWB Life 50:33-37(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 24;
1; Mismatches 1; Indels
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INIT MET 0 0 0 S4 RNA-BINDING.
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(Rel. 42, Last sequence update)
(Rel. 43, Last annotation update)
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75.0%;
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Matches 6; Conservative
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10-OCT-2003
15-MAR-2004
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                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine 5'-phosphate + H(2)0.
-!- SIMILARITY: Belongs to the pseudouridine synthase rlua family.
-!- SIMILARITY: Contains 1 S4 RNA-binding domain.
                                                                                                                                                  SEQUENCE OF 1-250 FROM N.A.
SUBJUNE-2000DP / ACC 700724,
STRAIN=3500DP / ACC 700724,
STRAIN=3500DP / ACC 700724,
SUB S., Schilling B., Tarantino L., Tullius M.V., Gibson B.W.,
Munson R.S. Jr.;
"Cloning and characterization of the lipooligosaccharide
"Cloning and characterization of the lipooligosaccharide
"Accosyltransferase II gene of Haemophilus ducreyl.";
J. Bacteriol. 182:229-2298(2000).
-:- FUNCTION: Responsible for synthesis of pseudouridine from uracil
at positions 1911, 1915 and 1917 in 23S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Relbosomal large subunit pseudouridine synthase D (EC 4.2.1.70)
(Pseudouridylate synthase) (Uracil hydrolyase).
                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
  large subunit pseudouridine synthase D (EC 4.2.1.70)
                                                                                             STRAIN=35000HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
Johnson L., Nguyen D., Wang J., Forst C., Hood L.,
"The complete genome sequence of Haemophilus ducrey.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.4%; Score 40; DB 1; Length 325; 75.0%; Pred. No. 24;
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InterPro; IPR006224; Rlu synth.
InterPro; IPR002942; S4.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE017152; AAP95428.1; -.
EMBL; AF224466; AAF32394.1; -.
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255 GRPRPPKG 262
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Best Local Similarity
6; Conserva
                                faemophilus ducreyi.
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                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GHPRPPRG
                                                                NCBI_TaxID=730;
                   RLUD OR HD0469
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RLUD_SALTY
ID_RLUD_SALTY
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STRAIN=CO-92 / Biovar Orientalis;
MEDLINE=2440413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdenor Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
Mature 413:523-527(2001).
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Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P. Perra N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.
                                                                                                                                                                                                                                                                  Gaps
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J. Bacteriol. 184-4601-4611(2002).
-!-FUNCTION: Responsible for synthesis of pseudouridine from uracil at positions 1911, 1915 and 1917 in 235 ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)
(Pseudouridylate synthase) (Uracil hydrolyase).
RLUD OR SFHB OR YP03277 OR Y0912.
                                                                                                                                                                                                71.4%; Score.40; DB 1; Length 325; 75.0%; Pred. No. 24; tive 1; Mismatches 1; Indels
rRNA processing, Lyase, RNA-binding, Complete proteome.
INIT MET 0 0 8 SIMILARITY.
DOMAIN 17 90 S4 RNA-BINDING.
ACT_SITE 138 138 BY SIMILARITY.
                                                                                                                                    7AFDDD9A1EDF91D9 CRC64;
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CTPAIN=KIMS / Biovar Mediaevalis;
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                                                                                                                                    325 AA; 36969 MW;
                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                    254 GRPRPPKG 261
                                                                                                                                                                                                                                                                                                                                     1 GHPRPPRG 8
                                                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserv
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STRAIN=12986/SvBVTac;
MEDLINE=22105643; PubMed=12110169;
Cole S.E., Levores J.M., Tilghman S.M., Vogt T.F.;
"Clock regulatory elements control cyclic expression of Lunatic fringe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
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009010; Q8K3F1; Q9DC10;
28-FEB-2003 (Rel. 41, Created)
10-0CT-2003 (Rel. 42, Last annotation update)
Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe (EC 2.4.1.222)
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STRATESTBL/65 TISSUE=Lung;
STRATN=CSTBL/65 TISSUE=Lung;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Fukunishi Y., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburar M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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MEDLINE=97330691; PubMed=9187150;
Johnston S.H., Rauskolb C., Wilson R., Prabhakaran B., Irvine K.D.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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"A family of mammalian Fringe genes implicated in boundary determination and the Notch pathway.";
Development 124:2245-2254(1997).
InterPro; IPR006145; PseudoU synth.
InterPro; IPR00624; Rlu_synth.
InterPro; IPR00624; Rlu_synth.
InterPro; IPR00624; Rlu_synth.
InterPro; IPR00649; PseudoU_synth_2; 1.
Pfam; PP00449; PseudoU_synth_2; 1.
ProDom; PD0041919; Psi Rlu; 1.
ITGRFAMS; TIGR00005; FluD_subfam; 1.
PROSITE; PS00129; Psi Rlu; 1.
PROSITE; PS00489; S4; Rlu; 1.
PROSITE; PS0089; S4; RNA-binding; Complete proteome.
IPRNA processing; Lyase; RNA-binding; Complete proteome.
DOMAIN 18 91 84 SIMILARITY.
SEQUENCE 325 AA; 36706 MW; F05D586CDD123ADF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 71.4%; Score 40; DB 1; Length 325; Similarity 75.0%; Pred. No. 24; 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase).
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Dev. Cell 3:75-84(2002)
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MEDLINE=22105642: Pubbled=12110168;
A MOTALES A.V. Yasuda Y., Ish-Horowicz D.;
Motales A.V., Yasuda Y., Ish-Horowicz D.;
Motales A.V., Yasuda Y., Ish-Horowicz D.;
Dy a cyclic transcriptional enhancer responsive to notch signaling.";
Dy a cyclic transcriptional enhancer responsive to notch signaling.";
Dr. Cell 3:63-74(2002).
In Motal Glycosyltransferace that initiates the elongation of O-
linked fucose residues attached to EGF-like repeats in the
extracellular domain of Notch molecules inhibiting Jagged mediated
Notch signaling. Bissential mediator of somite segmentation and
patterning. During somite Doundary formation, it restricts Notch
control of Notch and Committee as Section and patterning the presentic mediator of Somite segmentation and
cotivity in the presentic mesoderm to a boundary-formig territory
in the posterior half of the prospective somite. In this region,
Notch function activates a set of genes that are involved in
Control of the prospective somite involved in
Control of the prospective somite involved in
Control of the prospective monthment and promotes B
coll development in lymphoid progenitors. May play a role in
boundary formation of the enamel knot.
Contained from the proposition of the propos
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Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Badarelli R., Barrbi G., Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann W., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchiconni L., Mashima U., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasoki H., Schoenback C., Seya T., Shibata Y., Stock K.-F., Wynshiam-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Wynshiam-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Lunatic, Manic, and Radical fringe genes.";
Mamm. Genome 10:535-541(1999).
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Koch U., Laccombe T.A., Holland D., Bowman J.L., Cohen B.L., Egan S.E.
Quidos C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98352783; PubMed≥9690473;
Evrard Y.A., Lun Y., Aulehla A., Gan L., Johnson R.L.;
"Lunatic fringe is an essential mediator of somite segmentation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moran J.L., Johnston S.H., Rauskolb C., Bhalerao J., Bowcock A.M., Vogt T.F.;
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"Functional annotation of a full-length mouse cDNA collection.";
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"Subversion of the T/B lineage decision in the thymus by lunatic
fringe-mediated inhibition of Notch-1.";
Immunity 15:225-236(2001).
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CHARACTERIZATION.
MEDLINE=22157274; PubMed=12167404;
Mustonen T., Tuemmers M., Mikami T., Itoh N., Zhang N., Gridley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thesleff I.;
"Lunatic fringe, FGF, and BMP regulate the Notch pathway during
epithelial morphogenesis of teeth.";
Dev. Biol. 248:281-293(2002).
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MEDLINE=99272806; PubMed=10341080;
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                                                                                                     DEVELOPMENTAL STAGE: Developmental protein. During segmentation it shows a cyclic transcription pattern which is under the control of Notch. Expressed in the caudal region of the presontic mesoderm with each cycle corresponding to the formation time of one somite. In the dental epithelium it is detected at stage E13.5. The pattern of expression corresponds exactly to the formation of the enamel knot between late bud and early cap stages.

PTM: A soluble form may be derived from the membrane form by
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
16-ECT-2003 (Rel. 42, Last annotation update)
16-ECT-1,3-N-acety1glucosaminyltransferase lunatic fringe (EC 2.4.1.222)
(O_fucosylpeptide 3-beta-N-acety1glucosaminyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosyltransferase; Developmental protein; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                   similarity).
-!- Tissum SepEcificITY: Detected at 12.5 dpc in all tissues examined with the highest level observed in adult brain and spleen. Detected in the dental epithelium.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
GlcNAc to the fucose residue of a fucosylated protein acceptor.
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V -> M (IN REF. 4).
V -> I (IN REF. 4).
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CLEAVAGE (BY FURIN-LIKE PROTEASE)
(POTENTIAL).
                                                                                                                                                                                                                                                       proteolytic processing.
SIMILARITY: Belongs to the glycosyltransferase family 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 71.4%; Score 40; DB 1; Length 378; Best Local Similarity 100.0%; Pred. No. 28; Matches 6; Conservative 0; Mismatches 0; Indels
                     SUBCELLULAR LOCATION: Type II membrane protein. Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Itoh N.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL; AX124581; AAM93541.1; --
EMBL; AX04642; --
EMBL; AK004642; --
MGJ; MGI:1095413; Lfmg.
GO; GO:0007386; P:compartment specification; IMP.
InterPro; IPR003378; Fringe.
Pfan; PF0244; Fringe; 1.
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343
361
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86
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343
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378 AA;
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Q924T4;
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CONFLICT
CONFLICT
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                                                                                                                      use by non-profit institutions as long as its content is in no way and first and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=2166591, PubMed=11807986;

MEDLINE=2166591, PubMed=11807986;

MILLY Zhu X. Zh. X. Roullard J.M., Ambros P.F., Lamb B.J.,

Kuick R., Eckart M., Weinhausl A., Fonatech C., Hanash S.M.;

"Combined restriction landmark genomic scanning and virtual genome scans identify a novel human homeobox gene, ALX3, that is hypermethylated in neuroblastoma.";

I. Genes chromosomes Cancer 33:285-294(2002).

C. - FUNCTION: Transcriptional regulator with a possible role in patterning of mesoderm during development (By similarity).

C. - SURCEBLUIAR LOCATION: Nuclear [By similarity).

C. - SURCEBLUIAR Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALX3 HUMAN STANDARD; PRT; 343 AA.
095076; 095075;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Homeobox protein aristaless-like 3 (Proline-rich transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
VCPI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
SUBL-TYPE LECTIN 1.
SUBL-TYPE LECTIN 2.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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DR BME, AF38257, AAL40410.1;
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DR MGD, MGI:1918217; 49314084028ik.
DR InterPro; IPR000922; Gal_lectin.
DR PROSITE; PS50229; SUBL_LECTIN; 2.
DR Signal; Transmembrane; Repeat; Glycoprotein; Lectin.
Signal, Transmembrane; Repeat; Glycoprotein; Lectin.
Signal, Transmembrane; Repeat; Glycoprotein; Lectin.
Signal, 440 CYTOPLASMIC (Pr.
CHAIN 49 440 CYTOPLASMIC (Pr.
NNNEM 322 342 CYTOPLASMIC (Pr.
NNNEM 343 440 CYTOPLASMIC (Pr.
159 159 SUBL-TYPE LF.
168 260 SUBL-TYPE LF.
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AD514E7C7015D4F0 CRC64;
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100.0%; Pred. No. 30.
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nes 6; Conservative
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ALX3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstainnthe the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                   FUNCTION: Glycosyltransferase that initiates the elongation of O-
linked fucose residues attached to BGP-like repeats in the
extracellular domain of Notch molecules inhibiting Jagged mediated
Notch signaling. Essential mediator of somite segmentation and
patterning (By similarity).
CATALYTIC ACTIVITY: Transfers a beta-D-GloNAc residue from UDP-D-
GLONAC to the fucose residue of a fucosylated protein acceptor.
SUBCELLULAR LOCATION: Type II membrane protein. Golgi (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=21564202; PubMed=1170702;
Reymond A., Friedli M., Neergaard Henrichsen C., Chapot F.,
Rutonarakis S., Ucla C., Rossier C., Lyle R., Guipponi M.,
Antonarakis S.E.;
"From PREDs and open reading frames to cDNA isolation: revisiting the
human chromosome 21 transcription map.";
Genomics 78:46-54(2001).
-! TISSUE SPECIFICITY: Ubiquitcus.
-! SIMILARITY: Contains 2 SUEL-type
-! SIMILARITY: TO C.ELEGANS F32A7.3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003778; Fringe.
Pfam; PF02434; Fringe; 1.
Transferase; Glycosyltransferase; Developmental protein; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                   similarity).
-i- PTM: A soluble form may be derived from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL). 482A68ED60499066 CRC64;
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CLEAVAGE (BY FURIN-LIKE PROTEASE)
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28;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein C2lorf63 homolog precursor.
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Pred. No.
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378 AA;
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CU63 MOUSE
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DR HSSP, P06601; 1FJL.

DR TRANSFAC; T04515; -.

DR Genew, HONC:449; ALX3.

DR InterPro; 1PR00136; Homeobox.

DR InterPro; 1PR00136; Homeobox.

DR InterPro; 1PR00136; Homeobox.

DR ProDom; P0000010; Homeobox; 1.

DR PROSITE; PS000027; HOMEOBOX. 1.

DR PROSITE; PS000027; HOMEOBOX. 1.

DR PROSITE; PS000027; HOMEOBOX. 2; 1.

DR PROSITE; PS000027; HOMEOBOX. 1; 1.

AT Interprosition 1; 1.

DR PROSITE; PS000027; HOMEOBOX. 1.

DR PROSITE HOMEOBOX. 1.

DR PROSITE HOMEOBOX. 1.

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DR PROSITE HOMEOBOX. 1.

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Search completed: April 6, 2004, 16:08:00 Job time : 6.80374 secs

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                                                                    April 6, 2004, 15:51:34 ; Search time 32.5514 Seconds (without alignments) 87.236 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                               OM protein - protein search, using sw model
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Q8H3U2
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Q96IE7 Q96IE6 Q9AJP5 Q80TR1	Q9HAR3 097831 094910 088917 Q8WWN8 048926	Q94MU2 Q9H224 O57931 Q69124 Q69129	08X2S7 069145 098H39 004397 08AZK8 QBAZK6	Q8AZK4 Q8AZK3 Q8AZK2 Q8AZK1 Q8AZK0 Q69146	ALIGNMENTS	PRT; 268 AA.	a) equenc nnotat r) (Ta	opsida	tuber; T.; in the	nding; IEA. tin. 2.	12-A PROTEIN. 12-B PROTEIN. W; DCDE7355788D69FF
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Gaps

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Match 100.4%; Score 45; DB 10; Length 268; Local Similarity 100.0%; Pred. No. 17; or Conservative 0; Mismatches 0; Indels

g $\dot{\delta}$

SMART; SN NON TER CHAIN CHAIN SEQUENCE Query Match Best Loc Matches

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Bácteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                           Tuberculist; Rv1215c; ...

Tuberculist; Rv1215c; ...

R GO; GO:0003674; C:nucleus; IEA.

R GO; GO:0003677; F:nby brinding; IEA.

R GO; GO:001679; F:nby brinding; IEA.

R GO; GO:0006182; P:netabolism; IEA.

R GO; GO:0006182; P:netabolism; IEA.

R GO; GO:0006508; P:netabolism; IEA.

R InterPro; IPR008979; Gal bind peptidolysis; IEA.

R InterPro; IPR008979; Gal bind like.

R InterPro; IPR008939; Reptidace Sis.

R Ffam; PF02122; Peptidace Sis; I.
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PROSTIE; PS0037; MYB_1; 1.
Hypothetical protein; Hydrolase; Complete proteome.
Hypothet 561 AA; 62610 MW; 6D2C3253F2D3598D CRC64;
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Last sequence update)
Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
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MEDLINE=22709107; PubMed=12788972;
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EMBL; Z93777; CAB07817.1; -.
EMBL; AE007002; AAK45510.1;
PIR; E70610; E70610
TIGR; MT1253; -.
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005089;
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01-JUL-1997
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann J., DeBoy R., Dadson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=H37RY,
MEDINE=9825987, PubMed=9634230;
MEDINE=9825987, PubMed=9634230;
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Hornsby T., Jagels K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Feltwell T., Gentles S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitehead S., Squares R.,
Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.",
Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Diester hydrolase, putative).
RV1215C OR MTC1334.27C OR MTL253.
Mycobacterium tuberculosis.
Mycobacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corymebacterines, Mycobacterianes, Mycobacterium.
NCBL TAXID=1773;
                                                                                                                                                                                                                                                                                 STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Susaki T., Matsumoto T., PAC
close:P0418E08.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP004382; BAC16073.1;
SEQUENCE 407 AA; 43973 MW; D39ES77777F8252C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              / Match 80.4%; Score 45; DB 10; Length 407; Local Similarity 87.5%; Pred. No. 24; les 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561 AA.
                                                    407 AA
                                                  PRT;
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                                                    PRELIMINARY;
                                                                  Q8H3U2;
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 HPEPPRGR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 HPRPPRGR 9
                                                                                                                                    P0418E08.7 protein.
P0418E08.7.
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Gaps
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SECUENCE FROM N.A.
STRAIN-12822 / ATCC BAA-587;
MEDLINE-22827954, PubMed=12910271;
MEDLINE-22827954, PubMed=12910271;
Parkhill J., Sebaina M., Preston A., Murphy L.D., Thomson N.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerfenor-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2). Bacteria; Cyanobacteria; Chroococcales; Synechococcus. NCBI_TaxID=1140;
                                     DB 10; Length 862;
97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%; Score 42; DB 2; Length 181; 75.0%; Pred. No. 34;
                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0cT-2002 (TrEMBLrel. 22, Created)
01-0cT-2002 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
NugC (EC 1.6.5.3) (NADH dehydrogenase).
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AA
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                                                                                                             Mismatches
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                                         Score 43;
Pred. No.
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                                 76.8%;
77.8%;
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NCBI_TaxID=519;
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Best Local Similarity 75.0%
                                 Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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228 GYPYPPRGR 236
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                                                                                                                                                                                 1 GHPRPPRGR
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SEQUENCE FROM N.A.

STAIN=cv. Scorza verde;

Mita Gv. Scorza verde;

Mita Gv. Gallo A., Fasano P., Zasiura C., Casey R., Santino A.;

Mita Gv. Gallo A., Fasano P., Zasiura C., Casey R., Santino A.;

Mita Gv. Gallo A., Fasano P., Zasiura C., Casey R., Santino A.;

Mobility and Color and
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                                                                                                                                                                                                                                         STRAIN=IPO12069;
MEDLINE=5319311; PubMed=7596291;
MOIDEN I., Choi K., Yamashita M., Murooka Y.;
Molnar I., Choi K., Yamashita M., Murooka Y.;
Molacular cloning, expression in Streptomyces lividans, and analysis of a gene cluster from Arthrobacter somplex encoding 1-
ketoseteroid-DELTA.1-dehydrogenase, 3-ketosteroid-DELTA.5-isomerase and a hypothetical regulatory protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diadek J., Yamashita M., Murooka Y.;
"Cloning, sequencing and characterization of the downstream region of Kadlo operon of Arthrobacter simplex.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 293338; CAB07541.1; -.
Hypothetical protein.
SEQUENCE 545 AA; 57318 MW; 55F441EBD5E3A19E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Spermatophyta; Magnollophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Rosales, Rosaceae, Amygdaloideae, Prunus.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Lipoxygenase (EC 1.13.11.12).
                                 Nocardioides simplex (Arthrobacter simplex).
Bacteria, Actinobacteria, Actinobacteridae, Actinor
Propionibacterineae, Nocardioidaceae, Pimelobacter
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PROSITE; PS00081; LIPOXYGENASE 2; 1.
PROSITE; PS50095; PLAT; 1.
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Pfam; PF01477; PLAT; 1.
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SMART; SM00308; LH2; 1.
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SEQUENCE FROM N.A.
                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
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                                                                                                                                           NCBI_TaxID=2045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-IF012069;
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SEQUENCE 862
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08 W4X6

08 W4X6

09 W4X6

00 W4X6

01 - M

01 - M

01 - M

02 SPUN

03 SPUN

04 SEQU

08 SEX

RA Mita

RA GO;

DR EMB

DR EMB

DR PET

DR PET

DR PET

DR PET

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BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                           Adrenergic receptor alpha 2B.
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Matches 6; Conservative
                                                                                                                                                                                                            6; Conservative
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249 GHPKPPR 255
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249 GHPKPPR 255
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Matches 6; Conserv
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01-OCT-2003
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Q8T777
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Q925K6
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 Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Rabbinowitedh E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Salton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
"Comparative analysis of the genome sequences of Bordetella pertussis of the genome sequences of Bordetella pertussis, nat. Genet. 35:32-40(2003).

BMB., BKG4045; CAR40198.1;
"Hypothetical protein; Complete proteome.

BRD: BKG4018.1; "Hypothetical protein; Complete proteome.
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                                                                                                                                                                        Gaps
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Submitted (DEC-2000) to the EYBL/GenBank/DDBJ databases.
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                          75.0%; Score 42; DB 16; Length 259; 77.8%; Pred. No. 47; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.0%; Score 42; DB 2; Length 332; llarity 100.0%; Pred. No. 59; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-PCC 7942;
Trainoremas N.F., Golden S.S.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U444761; AAA86647.1; -.
InterPro; IPR001064; Crystallin.
PROSITE; PS00225; CRYSTALLIN_BETAGAMWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 AA; 38574 MW; CA17B5F4B0F2ED09 CRC64;
                                                                                                                                                                                                                                                                                                       vl-wov-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
08F11692 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adrenergic receptor alpha 2B.
                                                                                                                                                                                                                                                                                           332 AA.
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                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                          GEPRPPTGR 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
tes 7; Conserv
                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                 1 GHPRPPRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1140;
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SEQUENCE
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Matches
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Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J., Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.; Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.; High-Throughput Sequence Identification of Gene Coding Variants within Alcohol-related OTLs.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
- I- SIMILARITY: BELONGS TO PAMILY I OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;'
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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C -1-SIMILMARIA.

R MADI, AFRICAGO, AAKS6078.1; -.

R MADI, AFRICAGO,

R MOD, MOI:87935; AAKS6078.1; -.

R GO; GO:0004938; F:alpha2-adranergic receptor activity; IDA.

R GO; GO:000165; P:maprkK cascade; IMP.

DR HOPPO; IPR000276; GPCR_Rhodpsn.

PRINTS; PR00127; GPCR_Hodpsn.

DR PRINTS; PR00127; GPCR_HODPSN.

DR PROSITE; PS0127; GPCR_HODPSN.

DR PROSITE; PS0127; GPCR_HODPSN.

DR PROSITE; PS0127; GPCR_HODPSN.

R PROSITE; PS0127; GPCR_HODPSN.

DR PROSITE; PS0127; GPCR_HODPSN.

DR PROSITE; PS0127; GPCR_HODPSN.

R PROSITE; PS01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 42; DB 11; Length 448; 85.7%; Pred. No. 77; 11ve 1; Mismatches 0; Indels
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MOD; MOISTONES, Adra2D.

GO; GO:0001525, Pandiogenesis; IMP.

GO; GO:0001525, Pandiogenesis; IMP.

GO; GO:0001525, Pandiogenesis; IMP.

InterPro; IPR00276; GPCR_Rhodpsn.

PRIMITS; PR00027; GPCR_Hhodpsn.

PROSITE; PS000217; GPCRHHODPSN.

PROSITE; PS000237; GPROTEIN RECEP_F1_2; 1.

PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 448 AA; 49998 MW; B37E5E21B0EC4625 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 25, Last annotation update)
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SEQUENCE FROM N.A.

STRAIN=CSTBL/6; TISSUE=Brain;

KATAN=CSTBL/6; Marusina F.S., Wagner L., Shenmen C.M., Schuler G.D.,

KATAN=CSTBLETON N. More T., Max S.I., Wang J., Hong L.,

KATAN=CSTBLETON N., Solars M.B., Bondaldo M.F., Caraninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

KATCHARGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

KATCHARGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

KATCHARGS M.M. Touchman J.W., Green E.D., Dickson M.C.,

Radriguez A.C., Garimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,

KATCYWINSKI M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Splicing factor proline/glutamine rich (Polypyrimidine tract binding protein associated).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 42; DB 4; Length 707; 85.7%; Pred. No. 1.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Strausberg R.;
Submitted (ARR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051192; AAH51192.1; -
GO, GO:000376; F:nucleic acid binding; IEA.
InterPro: IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
SWART: SW00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS50102; RRM; 2.
SEQUENCE 707 AA; 76188 MW; B5C287EF61FD1811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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STRAIN=C57BL/6; TISSUE=Brain;
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                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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Q7TNES;
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               SO DE REPRENCIO DE LA PROPERTA DE LA PRENCIO DE LA PRENCIO
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Eukaryota, Viridiplantae, Streptophyra, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Abi-Rached L., Gilles A., Shiina T., Pontarotti P., Inoko H.;
Abi-Rached L., Gilles A., Shiina T., Pontarotti P., Inoko H.;
Bytachec of en bloc duplication in vertebrate genomes.";
I Nat. Genet. 0.0-0(2002).

EMBL, AF391288; AAM18867.1;
EMBL, AF391288; AAM1867.1;
RGO, GO:0016491; F:Oxidoreductase activity; IEA.

RGO, GO:0016491; F:Oxidoreductase centre.

R InterPro; IPR002227; TYrosinase.

R Pfan; PP00264; tyrosinase;
R Pfan; PP00264; tyrosinase;
R Pfan; PR00379; TYROSINASE.

R PROSITE; PS00499; TYROSINASE.

R PROSITE; PS00499; TYROSINASE_2; 1.
                                                                   Hypotherical protein.
Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
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STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome B, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 42; DB 10; Length 535; llarity 100.0%; Pred. No. 91; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 75.0%; Score 42; DB 5; Length 494; Local Similarity 87.5%; Pred. No. 85; lonservative 0; Mismatches 1; Indels
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, PA005504; BAC57819.1; -.
Inter.Pro. IPR002885; PPR.
Pfam; PF01555; PPR; 8.
TIGRFAMS; TIGR00756; PPR; 9.
SEQUENCE 535 AA; 58557 MW; C2712C4178582382 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56646 MW; 6823A97CDCFA105E CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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SEQUENCE 494 AA; 5
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                         NCBI_TaxID=7739;
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Best Loca Matches

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RESULT 13 Q84SD0

Strausberg R.;

707 AA.

PRT;

PRELIMINARY;

Q86VG2

RESULT 14 Q86VG2 ID Q86VG

; 0

Gaps

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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL, BC055793; AAH55793.1; -. Hypothetical protein.

NOM TER 1 1 SEQÜENCE 322 AA, 33966 MW, 9B7D23E6FE505774 CRC64;
       RL
DR
KW
KW
SQ
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0; Gaps Query Match 73.2%; Score 41; DB 11; Length 322; Best Local Similarity 77.8%; Pred. No. 83; Matches 7; Conservative 0; Mismatches 2; Indels

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Search completed: April 6, 2004, 16:14:41 Job time : 32.6283 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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April 6, 2004, 15:29:39; Search time 50.3832 Seconds (without alignments) 50.472 Million cell updates/sec Run on:

US-10-009-709-8 56 Title: Perfect score:

1 GHPRPPRGR 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04: geneseqp1980s:* Database :

geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

	g :	Human sal	Human sal	Human sal	Peptide #	Peptide #	Human bon	Human bra	Human liv	Human pep	Human NOV	Human sec	Human PRH	Human sal	Human sal	Propionib	Propionib	Propionib	Streptomy	Germline	Novel hum	Zea mays	Human EST	Human EST	Human EST	Propionib
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	Description	4ab4877	Aab4877	4ab4878	Abb3884	O	in	Aam5949	Abg5374	Abg4187	Abr5742	Abr5676	Ada8379	Adc98216	Aab4877	Abm6579	Aau6574	Abm6226	Abp76681	Aay65870	Abg28896	Aag58448	Aam2383	Aam23850	Aam2401	Aau4974
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SUMMARIES	ID	AAB48778	AAB48777	AAB48783-	ABB38848	AAM32323	AAM72058	AAM59494	ABG53742	ABG41873	ABR57423	ABR56769	ADA83798	ADC98216	AAB48779	ABM65798	AAU65747	ABM62266	ABP76681	AAY65870	ABG28896	AAG58448	AAM23839	AAM23850	AAM24011	AAU49746
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ABM46265 AAB48780 ABB42253	AAM36062 AAM75953 AAM63140	ABP80084 AAU59993 ARM56512	AAU59580 ABM56099 AAU45247	ABM41766 ABG18278 AAU48625	ABG26281 ABG03818 ADE07941
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ALIGNMENTS

AAB48778 standard; peptide; 9 AA. 09-MAR-2001 (first entry) AAB48778; RESULT 1 AAB48778

Human saliva PRP-1 fragment (residues 100-108), SEQ ID NO:8.

Human; PRP-1; proline-rich protein; saliva; dental caries; chromosome 12p13.2; arginine catabolism; ammonia production; pH increase; oral bacterium; caries prevention.

Homo sapiens.

WO200069890-A1.

23-NOV-2000.

11-MAY-2000; 2000WO-SE000930.

99SE-00001773. 17-MAY-1999;

(STRO/) STROEMBERG N. (JOHA/) JOHANSSON I.

Stroemberg N, Johansson I;

WPI; 2001-031923/04.

New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.

Claim 4; Page 24; 36pp; English

The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPS (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-

RESULT 2 AAB48777

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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-derived oligopeptides of the invention
                                                                                                                                                                                                                      Human, PRP-1; proline-rich protein, saliva, dental caries,
chromosome 12p13.2; arginine catabolism, ammonia production, pH increase,
oral bacterlum, caries prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligopeptides comprising 2 arginine residues from degradation of
proline-rich proteins, useful for preventing dental caries.
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                                                                                                                                                                              Human saliva PRP-1 fragment (residues 99-115), SEQ ID NO:13
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                                                       AAB48783 standard; peptide; 17 AA.
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                                                                                                                                         (first entry)
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                 AAB48783;
                 RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, PRP-1; proline-rich protein, saliva; dental caries;
chromosome 12p13.2; arginine catabolism; ammonia production; pH increase;
oral bacterium; caries prevention.
                                                                                                                       Gaps
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                                                                             100.0%; Score 56; DB 4; Length 9; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
derived oligopeptides of the invention
                                                                                                                                                                                                                                                                                                               AAB48777 standard; peptide; 10 AA.
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                                                           Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHPRPPRGR 10
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                                       Sequence 9 AA;
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Gaps ; 0

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Best Loca Matches

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Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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100.0%; Pred. No. 0.97;
iive 0; Mismatches
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                                                                                                             Rank DR;
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                                                                       (MOLE-) MOLECULAR DYNAMICS INC
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               27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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21-SEP-2000; 2000US-0234687P.
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21-SEP-2000; 2000US-0234687P
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 132 AA;
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                                                                                                           Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
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Clarity 100.0%; Pred No. 0.97;
Conservative 0; Mismatches 0; Indels
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                                                                                                                                                          04-FEB-2000; 2000US-0180312P.
26-NMX-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000US-023559P.
                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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; 2000US-0207456P.
; 2000US-00608408.
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les 9; Conserv
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                                                 WO200157277-A2
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
               Homo sapiens.
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Matches

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RESULT 5 AAM32323

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Gaps

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ABG53742 standard; peptide; 132 AA

ABG53742

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GHPRPPRGR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human brain expressed single exon probe encoded protein SEQ ID NO: 31599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                    Gaps
                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO 31599; 650pp + Sequence Listing; English.
                                                                                                                                    100.0%; Score 56; DB 4; Length 132; Lonsity 100.0%; Pred. No. 0.97; Conservative 0: Mismatched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                   AAM59494 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US000667,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-0353599.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000; 2000US-0207456P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000; 2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the probes of the invention
                                                                                                                                                                                                                                                   GHPRPPRGR 90
                                                                                                                                                                                                                   σ
                                                                                                                                 Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483446/52
                                                                                                                                                                                                                   1 GHPRPPRGR
                                                                                                                   Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        brains.
                                                                                                                                                                                                                                                                                                  RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                        Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 56; DB 4; Length 132; Best Local Similarity 100.0%; Pred. No. 0.97; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 32390; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                          Human liver peptide, SEQ ID No 32390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG41873 standard; peptide; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                2000US-00608408.
                                                                                                                                                                                                                                                                                                                                               2000US-00632366.
2000US-0234687P.
                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GHPRPPRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 132 AA;
                                                                                                                                                                                                       WO200157273-A2
                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
                                                            25-FEB-2003
                                                                                                                                                                                                                                     09-AUG-2001
                              ABG53742;
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ABG41873
ID ABG4
a
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Gaps

.. 0

100.0%; Score 56; DB 4; Length 132; 100.0%; Pred. No. 0.97; ative 0; Mismatches 0; Indels

Conservative

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Matches

Query Match Best Local Similarity

1 GHPRPPRGR 9

Tue Apr

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ABG41873;
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(first entry)

Human peptide encoded by genome-derived single exon probe SEQ ID 31538

Human; single exon probe; asthma; lung cancer; CODD; LLD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histocytosis; lymphangioleiomyomosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocyetic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.

Homo sapiens.

15-NOV-2001

30-JAN-2001; 2001WO-US000665

; 2000US-0180312P. ; 2000US-0207456P. ; 2000US-00608408. ; 2000US-00323468. ; 2000US-0234687P. 04-FEB-2000; 26-MAY-2000; 30-JUN-2000; 2

03-AUG-2000; 21-SEP-2000; 27-SEP-2000;

04-OCT-2000; 2000GB-00024263

(MOLE-) MOLECULAR DYNAMICS INC

Rank DR; Chen W, Hanzel DK, Penn SG,

WPI; 2002-114183/15

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Claim 27; SEQ ID NO 31538; 634pp; English.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung compitating single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exors in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably albeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon show and (b) measuring the expression of each of the exons in several comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon several comprising the exons should be assigned to a single gene; a peptide comprising of the exons should be assigned to a single gene; a peptide comprising compression of the exons in the tissues and/or cell types using hybridisation, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human analysis, and for identifying exons in a gene, particularly using human analysis, and for the study of lung diseases such as athma, lung derived manalysis, and for the study of lung designed to a single

New NOVX polypeptide useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.

WPI; 2003-140359/13. N-PSDB; ACF03558

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tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histocytosis, lymphangiolelomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; NOVX, cytostatic; cardiant; antiinflammatory; immunosuppressive; antiallergic; haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; antiarteriosclerotic; antiarteriosclerotic; neuroscotic; antiarteriosclerotic; neuroprotective; nootropic; antibacterial; virucide; antiparasitic; relaxant; anticonvulsant; hypotensive; vasotropic; antiparkinsonian; vulnerary; angiogenic; antiangiogenic; gene therapy; vaccine; cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma; acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis; Alzheimer's disease; Parkinson's disease; goitre; infection; stroke; muscular dystrophy; epilepsy; wasting disorder; chromosome 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MM. Macdougall JR, Smithson G, Millet I, Stone DJ;
E, Ellerman K, Alsobrook JP, Lepley DM, Burgess CE;
G, Edinger SR, Gangolli EA, Gorman L, Taupier RJ, Li L;
Rernandes ER, Vernet CAM, Tchernev VT, Casman SJ, Shenoy S;
/, Furtak K, Baumgartner JC, Colman SD;
                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                                                                                                                                                                 100.0%; Score 56; DB 5; Length 132; 100.0%; Pred. No. 0.97; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR57423 standard; protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human NOV7 protein SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-NOV-2000; 2000US-0245291P.

02-NOV-2000; 2000US-0245652P.

08-NOV-2000; 2000US-0246652P.

08-NOV-2000; 2000US-0246871P.

26-UAN-2001; 2001US-026438P.

26-UAN-2001; 2001US-026423P.

29-UAN-2001; 2001US-026423P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-NOV-2001; 2001WO-US051580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                   82 GHPRPPRGR 90
                                                                                                                                                                                                                                                                                                            1 GHPRPPRGR 9
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                                                                                                                                                                                              Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200294870-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grosse WM,
Gunther E,
Spytek KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2002
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Mishra V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR57423;
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; gene therapy; cancer; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allergy; AIDS; inflammatory disorder; developmental disorder; hypothyroidism; Cushing's syndrome; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; SECP; cytostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein SECP-44 SEQ ID NO:44.
                                                                                                                                                                                                                                                                                                                                            ABR56769 standard; protein; 154 AA.
         Claim 1; Page 69; 346pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-0317824P.
2001US-0324040P.
2001US-0324586P.
2001US-03343980P.
2001US-0334229P.
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2001US-0314752P.
2001US-0317818P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002US-0362439P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-AUG-2002; 2002WO-US027143
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                 GHPRPPRGR 107
                                                                                                                                                                                                                                Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                               1 GHPRPPRGR 9
                                                                                                                                                                                                                         Sequence 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003016506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-SEP-2001;
02-NOV-2001;
28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                               ABR56769;
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                                                                                                                                                                                                                                                                                                                           RESULT 11
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human; marker; expressed sequence tag; EST; arabidopsis; tumour; stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;

30-MAY-2002; 2002WO-IB004189.

WO2002103028-A2.

27-DEC-2002.

Homo sapiens.

vaccine.

THE STANDARD STANDARD

2001US-0293999P. 2001US-0330457P.

30-MAY-2001; 22-OCT-2001;

2002US-0376988P

19-MAR-2002

ADA83798 standard; protein; 166 AA.

RESULT 12 ADA83798 (first entry)

20-NOV-2003

ADA83798;

Human PRH2 protein.

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100.0%; Score 56; DB 6; Length 154; 100.0%; Pred. No. 1.1; tive 0; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Matches 9; Conserv

Sequence 154 AA;

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ACT 99126 to ARC59105 encode the human secreted proteins (I) given in ABR56726 to ABR56805, designated SECP-1 to SECP-80. SECP sequences can harbstatic, antiarterisoclerotic, anticonvulsant, antialflammatory, nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic and thyromimetic activities, and can be used in gene therapy. The SECP proteins and polymucleotides can be used in diagnosing, treating and preventing diseases or conditions associated with the decreased or proteins and polymucleotides can be used in diagnosing, treating and preventing diseases or conditions associated with the decreased or expression or overexpression of SECP, such as cell proliferative (e.g. expression or overexpression of SECP, such as cell proliferative (e.g. cancer, atherosclerosis), immune/inflammatory (e.g. AIDS, allergies) and disease, stroke, immune/inflammatory (e.g. AIDS, allergies) and campounds on the expression of nucleate acid and anino acid sequences of SECP. The SECP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                        New human secreted proteins (SECP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant SECP expression e.g. cancer, AIDS, atherosclerosis, Huntington's disease, stroke, infections.
                                                                                       ren BA, Gietzen KJ, Lal PG, Yue H, Honchell CD;
Burford N, Xu Y, Baughn MR, Duggan BM, Tran UK;
/the IJ, Richardson TW, Lee S, Thangavelu K, Yue H
Walia NK, Azimzai Y, Sanjanwala B, Hafalia AJA;
Nguyen DB, Ison CH, Astromoff A, Ding L, Lee SY;
nkumar J, Gandhi AR, Jin P, Fu GK, Swarnakar A;
                                                                  Lehr-Mason PM, Burford N, Xu Y, Bau
Lee EA, Forsythe IJ, Richardson TW,
Emerling BM, Walia NK, Azimzai V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 222; 286pp; English.
                           (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                              Ramkumar J,
                                                                                                                                                                                                                                                                                                                         WPI; 2003-278569/27.
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ACC79069
                                                                                                                                                                                                                               Borowsky M
Becha SD,
ACK ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABR57412 to ACF03547 to ACF03570 encode the human NOVX proteins (I) have cytostatic, cardiant, antinflammatory, nootropic, immunosuppressive, antiallary, antidiabetic, antiatrearlosclerotic, antiathmatic, antiathmatic, reputedict, antiathmatic, notropic, antiparterial, relaxant, antiparasitic, netronvalsant, hypotensive, antibacterial, relaxant, antiparasitic, anticonvalsant, hypotensive, antibacterial, relaxant, cartiparasitic, anticonvalsant, hypotensive, antibacterial, relaxant, of antiparasitic, anticonvalsant, hypotensive, and can be used in gene therapy and vaccines. The NOVX polypeptides and their antibodies can be used to determine the presence or absence of (I) in a sample. The NOVX polypeptides, polymocleotides encoding them, and antibodies against them, are useful in manufacturing a medicament for treating or preventing a syndrome associated with a NOVX-associated disorders, asthma, inflammation, cardiomyopathy, atheroscleosis, blood disorders, obesity, acquired immunodeficiency syndrome (ADS), immunoglobulin (Ig) A nephropathy, clirchosis, arthritis, Alzheimer's disease, Parkinson's disease, actions, and other wasting disorders associated with chronic diseases. ACF03571 to ACF03544 stopersent por present invention sequence, which are used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 56; DB 6; Length 149; 100.0%; Pred. No. 1.1; tive 0; Mismatches 0; Indels
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04-APR-2003; 2003WO-JP004325.
                                                                                                                                                                                                                                                                                     08-APR-2002; 2002JP-00105425
               Baranova AV, Yankovsky NK,
                                                                                                                                                                                                              01-JAN-2004 (first entry)
                                                                                                                                                Ouery Match
Best Local Similarity 100.
       (BIOM-) BIOMEDICAL CENT
                                                                                                                                                                   1 GHPRPPRGR 9
                       WPI; 2003-175241/17.
N-PSDB; ADA83797.
                                                                                                                                                                                                                                          risk assessment;
antiinflammatory.
                                                                                                                                            Sequence 166 AA;
                                                                                                                                                                                                                                                             WO2003084991-A1
                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                     16-OCT-2003
                                                                                                                                                                                                       ADC98216;
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                                              cissue.
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The invention relates to the human atopic dermatitis-inducing proteins, salivary acidic proline-rich phosphoprotein (PRP; ADC92216) and prolactin chandrale protein (PIP; ADC9218), and their post-translationally modified forms. These proteins are secreted by salivary or sweat glands and bind to IgE autoantibodies, thereby activating mast cells and bind to IgE autoantibodies, thereby activating mast cells and proper properties or lates to antigenic peptide fragments of PRP or PIP; antibodies which bind to PRP or PIP; methods for diagnosing atopic dermatities by determining the presence of PRP- or PIP-specific antibodies or immune complexes, or by quantifying histamine release; and sensitisation remedies for atopic dermatities on their peptides as the active injected. PMP, PIP and their antibodies are useful in diagnosing atopic dermatities. Or for determining whether an individual is at risk of developing atopic dermatitie. They are also useful in diagnosing actopic dermatitie. They atopic dermatities. The present sequence represents the specifically actopic dermatities. The present sequence represents the specifically claimed human salivary acidic proline-rich phosphoprotein (PRP).
                                                                                                                                                                                  Atopic dermatitis-inducing proteins, applicable in diagnosis of including risk of onset, and in developing sensitization remedies for the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, PRP-1; proline-rich protein, saliva, dental caries,
chromosome 12p13.2; arginine catabolism, ammonia production, pH increase,
oral bacterium, caries prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human saliva PRP-1 fragment (residues 101-108), SEQ ID NO:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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100.0%; Pred. No. 1.2;
iive 0; Mismatches
                                                   Tanaka T, Koro O;
                                                                                                                                                                                                                                                                      Claim 4; SEQ ID NO 2; 43pp; Japanese.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB48779 standard; peptide; 8 AA.
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Best Local Similarity 100.vv
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                                                   Hide M, Yamamoto S,
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                                                                                                       WPI; 2003-833567/77.
N-PSDB; ADC98215.
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                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (1871s) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue of interest hat are preferentially expressed in the phenotype/cell type of interest had a marker for a predetermined phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably arbidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting the absence or presence of peptides encoded by tumour associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a tumour associated antigen of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, salivary acidic proline-rich phosphoprotein, FRP, autoantigen, atopic dermatitis-inducing protein, salivary gland; ISB autoantibody; immunoglobulin E, mast cell activation, basophil activation; diagnosis, risk assessment; sensitiastion remedy; dermatological; antiallergic,
                                                                                                                                                                                                                                         Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
                                                                                                          Lobashev AV, Krukovskaya LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                          Kozlov AP,
                                                                                                                                                                                                                                                                                                                                                                                Claim 29; Page 191-192; 516pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC98216 standard; protein; 166 AA.
19-FEB-2002; 2002US-0357144P
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Gaps ö New oligopeptides comprising 2 arginine residues from degradation of

Stroemberg N, Johansson I;

WPI; 2001-031923/04.

(JOHA/) JOHANSSON I.

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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12pl3.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oard bacteria for mutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a bropionibacterium annes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM6436) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host comprising a additionally encompasses expression vectors and host comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; and polyneptides of the invention; and polyneptide of the invention; and polyneptides of the invention; and polyneptide of the invention; and polyneptides of the poly
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   proline-rich proteins, useful for preventing dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 8; 1.4e+06;
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Benson DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 derived oligopeptides of the invention
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Zhang Y, Wang S, Jen S, Lodes MJ,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABM65798 standard; protein; 92 AA.
                                                             Claim 4; Page 24; 36pp; English
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ABM65798
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Maisonneuve JL; Jones R, Carter D;

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method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations, or antigan-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a proteins, T cell populations or antigan-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnes polypeptides are useful for diagnosing, preventing or treating acnes protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the crimilation of an immune response against P. acnes polypeptide which is sequence represents a specifically claimed P. acnes polypeptide which is thought to contain an immunogenic region. Note: The sequence data for the primed in electronic forma part of the printed specification, but was the various or the vari
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88.9%; Pred. No. 19;
iive 0; Mismatches 1; Indels
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Matches 8; Conservative
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2004, 16:14:50; Search time 35.3271 Seconds (without alignments)

Fitle: US-10-009-709-8

Sequence: 1 GHPRPPRGR 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1071772 seqs, 262633353 residues

Total number of hits satisfying chosen parameters: 1071772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Published Applications AA:*

| cgn2_6/ptodata/1/pubpaa/DC7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/DC7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/DC7_NEW_PUB_pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_pep:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_pep:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_pep:*
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| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_P

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 43644, A	Sequence 7, Appli Sequence 69167, A	Sequence 43478, A	Sequence 45389, A Sequence 223703,	Sequence 6, Appli	Sequence 285441,	Sequence 192013,	Sequence 35, Appl	Sequence 2445, Ap	Sequence 1, Appli	Sequence 522, App
SUMMARIES	US-10-157-031-80	US-10-084-846A-7 US-10-425-114-69167	US-10-425-114-43478	US-10-864-761-45389 US-10-424-599-223703	US-10-084-846A-6	US-10-424-599-285441	US-10-424-555-152015 US-10-112-944-336	US-10-312-187-35	US-10-104-047-2445	US-08-811-519A-1	US-10-225-567A-522
DB	6 4 1	12	17	173	75	2 5	177	14	15	œ	14
% Query Match Length DB	1000	19652 238	277	40 72	19662	40.	433	550	747	1471	1474
% Query Match	100.0	82.1 80.4	80.4	75.0	75.0	73.2	73.2	73.2	73.2	73.2	73.2
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Sequence 914, Appli Sequence 114, Appli Sequence 114, Appli Sequence 1114, Appli Sequence 10259, A Sequence 10259, A Sequence 10259, A Sequence 141375, A Sequence 178111, A Sequence 239118, Sequence 239118, Sequence 239118, Sequence 241354, A Sequence 24134, A Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 128, Appli Sequence 128, Appli Sequence 128, Appli Sequence 2911, Appli Sequence 2911, Appli Sequence 2281, Appli Sequence 29711, A	9 15 24
15 US-10-292-798-914 16 US-09-870-154-8 17 US-09-870-154-8 18 US-09-871-798-114 19 US-09-815-742-10259 19 US-09-815-742-10259 10 US-09-815-742-10259 10 US-09-815-742-10259 10 US-09-815-742-10259 11 US-10-424-19847 12 US-10-424-599-178811 12 US-10-424-599-268692 12 US-10-424-599-268692 12 US-10-424-599-268692 12 US-10-424-599-268692 13 US-09-821-687-10 14 US-10-2821-687-10 15 US-10-2821-687-10 16 US-09-821-687-10 17 US-09-821-687-10 18 US-09-821-687-10 19 US-09-821-687-10 10 US-09-821-687-10 11 US-10-424-599-285656 12 US-10-424-599-285656 12 US-10-424-599-285656	US-10-424-599-15052 US-10-424-599-24603
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ALIGNMENTS

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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Wucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Streptomyces viridochromogenes
FEATURE:
OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 2.
OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
US-10-084-846A-7
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, OTHER INFORMATION: Clone ID: UC-ZMFLMO17307C10_FLI.pep
US-10-425-114-69167
                                                                              APPLICANT: MUTHENNEG, AGNES
APPLICANT: MTERFEER AARL
APPLICANT: RERFEER AARL
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFRENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US/TEP01/09815
PRIOR PLILING DATE: 2001-08-24
PRIOR PLILING DATE: 2001-08-24
PRIOR PLILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFFWARE: PATENTIN VET: 3.2
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 43478, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                             APPLICANT: WEITNAUER, GABRIELE
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ORGANISM: Zea mays
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US-10-425-114-43478
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LENGTH: 238
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LENGTH: 19652
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GENERAL INFORMATION:
APPLICANT: Bardoveky, N. K.
APPLICANT: Yankoveky, N. K.
APPLICANT: Lobashev, A. P.
APPLICANT: Lobashev, A. V.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences FILE REFERENCE: 2760-103
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OTHER INFORMATION: EXPRESSED IN PLACENIA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG. SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BARROW, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: SYNISSPROT HIT: BF088788.1, EVALUE 1.00e-01
US-09-864-761-43644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 56; DB 9; Length 132; Best Local Similarity 100.0%; Pred. No. 2; . Matches 9; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.11
SEQ ID NO 43644
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CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SEQ ID NO 80
LENGTH: 166
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US-10-084-846A-7
; Sequence 7, Application US/10084846A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-157-031-80
; Sequence 80, Application US/10157031
; Publication No. US20030108890A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: FRT
ORGANISM: Homo sapiens
FEATURE:
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US-10-157-031-80
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Best Local Similarity
Matches 9; Conserv
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Sequence 223703, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: About Xinua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE REPERENCE: 38 -21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 223703

LENGTH: 72
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.55

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN BONE MARROW SIGNAL = 0.61

US-09-864-761-45389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.0%; Score 42; DB 9; Length 40; Best Local Similarity 87.5%; Pred. No. 55; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_44033C.1.pep
US-10-424-599-223703
                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION UNBER: 2000-09-21
PRIOR APPLICATION UNMER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
PRIOR PILING DATE: 2011-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 45389
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APPLICANT: WUHLENNEG, ACARES
APPLICANT: TREFZER, AAE
APPLICANT: BECHTHOLD, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GHPRPPRG 8
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US-10-084-846A-6
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: CHEM, Wensheng
TITLE OF INVENTION: HIMMAN GENEE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: HIMMAN GENEE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICANTON NUMBER: US (0)180,312
RAIOR APPLICANTON NUMBER: US (0)180,312
RAIOR PILING DATE: 2000-02-04
RAIOR APPLICANTON NUMBER: US (0)666
RAIOR APPLICANTON NUMBER: US (0)666
RAIOR FILING DATE: 2000-00-09-27
RRIOR FILING DATE: 2000-00-09-27
RRIOR APPLICANTON NUMBER: US (0)20,456
RRIOR FILING DATE: 2000-10-130
RRIOR APPLICANTON NUMBER: US (0)20,466
RRIOR APPLICANTON NUMBER: US (0)20,0666
RRIOR APPLICANTON NUMBER: US (0)20,00-67
RRIOR APPLICANTON NUMBER: PCT/US01/00666
RRIOR APPLICANTON NUMBER: PCT/US01/00666
RRIOR APPLICANTON NUMBER: PCT/US01/00669
RRIOR PLING DATE: 2001-01-30
RRIOR PRING APPLICATION NUMBER: PCT/US01/0663
RRIOR PLING DATE: 2001-01-30
RRIOR PRIOR PLING DATE: 2001-01-30
RRIOR PRIOR PLING DATE: 2001-01-30
RRIOR PLING DATE: 200
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US-10-425-114-43478
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhao, Qing A. APPLICANT: Zhao, Qing A. APPLICANT: Wang, Zhiwei TITIE OF INVENTION: No. US20040048249Alel Nucleic Acids and TITLE OF INVENTION: Secreted Polypeptides FILE REPERENCE: 805A
                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_15954C.1.pep
US-10-424-599-192615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 8054
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR PILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR PILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-02-03
PRIOR PILING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-05-18
NUMBER: OF SEQ ID NOS: 924
SEQ ID NO 336
LENGTH: 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-112-944-336
. Sequence 336, Application US/10112944
. Publication No. US20040048249A1
. GENERAL INFORMATION:
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 192615
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Wehrman, Tom
Ghosh, Malabika
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Best Local Similarity 85.7
Watches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Gezhi
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Zhang, Jie
Ren, Feiyan
Xue, Aidong J.
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Zhao, Qing A.
Wang, Zhiwei
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; ORGANISM: Homo sapiens
US-10-112-944-336
                                                                                                                                                                                                                                                                                                                                           1 GHPRPPRGR 9
                                                                                               TYPE: PRT
ORGANISM: Glycine max
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68 GHPRPPQ 74
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                                                                                                                                                  FEATURE:
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Sequence 285441, Application US/10424599

Publication No. US20040031072A1

Sequence 28541, Application US/10424599

Publican No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILLE REPRENCE: 38-21(5223)8

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 285441
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
ITILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERRICE: 38-21 (53223)
CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.2%; Score 41; DB 12; Length 94; 77.8%; Pred. No. 1.6e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_99782C.1.pep
US-10-424-599-285441
                    FILE REFERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin Ver. 3.2
SOFTWARE: Patentin Ver. 3.2
       TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 77.8
Watches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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US-10-424-599-192615
                                                                                                                                                                                                                                                                                             TYPE: PRT
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APPLICANT: Petrenko, Alexandre
TITLE OF INVENTION: CALCIUM INDEPENDENT RECEPTOR OF
TITLE OF INVENTION: ALPHA-LATROTOXIN, CHARACTERIZATION AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Ploor
CITY: Hackensack
STRIET: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.2%; Score 41; DB 8; Length 1471; 77.8%; Pred. No. 1.7e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,519A
FILING DATE: 4-MAR.1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REFERENCE/DOCKET NUMBER: 1049-1-007
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1471 amino acids
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
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CORGANISM: Homo sapiens
US-10-225-567A-522
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TOPOLOGY: lin
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                                                                                                                                 APPLICANT: BENAED, Claire
APPLICANT: BENAED, Claire
APPLICANT: BENAED, Claire
APPLICANT: MCCRIGHT, Brent
APPLICANT: LAKOWGRI, Bernard
APPLICANT: HAN, Dong
APPLICANT: HANBER: US.
TITLE OF INVENTION: CLK-2, CKX-7 AND COQ-4 GENES, AND USES THEREOF
FILE REFERENCE: 11202-008-999
CURRENT APPLICATION NUMBER: US 60/254,932
PRIOR APPLICATION NUMBER: US 60/254,932
PRIOR PILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 60/213,174
PRIOR PELING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FRAESEQ for Windows Version 4.0
LENGTH: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2445.7

Publication No. US20030236392A1

GENERAL IRPORATION:

APPLICANT: HELLY RESERRCH INSTITUTE

TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA

FILE REPERRECE: H1-A0105

CURRENT APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE: 2002-03-25

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patentin Ver. 2.1

LENGTH: 747
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Pred. No. 7.3e+02;
0; Mismatches 2; Indels
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Pred. No. 9.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: XE7, Homo sapiens cex-7 protein US-10-312-187-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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                                                                     Sequence 35, Application US/10312187
Publication No. US20030162291A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.2%;
85.7%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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CRGANISM: Homo sapiens
US-10-104-047-2445
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Best Local Similarity
Matches 6; Conserv
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FEATURE:
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US-10-104-047-2445
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US-08-811-519A-1
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Sequence 522, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Burner, Glenna C.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: 60/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
SROID NOS: 2292
SOFTWARE: Parentin version 3.1
SEQ ID NOS: 2292
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Search completed: April 6, 2004, 17:06:06 Job time: 42.3271 secs

ein - secore secore secore secore secore secore secore secore secore	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	protein search, using sw model	April 6, 2004, 15:52:34 ; Search time 8.97196 Seconds (without alignments) 85.771 Million cell updates/sec	US-10-009-709-9 2: 50 1 HPRPPRGR 8	s: BLOSUM62 Gapop 10.0 , Gapext 0.5	283366 segs, 96191526 residues	of hits satisfying chosen parameters: 283366	eq length: 0 eq length: 200000000	Ing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	PIR 78:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	io. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.	SUMMARIES	Query Match Length DB ID De	0 100.0 166 1 PIHUSC salivary	0 100.0 166 2 B25372 salivary	4 88.0 561 2 E70610	1 82.0 2796 2 JC4743 fatty-ac	0 80.0 129 2 F/1241 0 80.0 691 2 A54741 erythrod	9 78.0 200 2 855609	9 78.0 346 Z 148185 9 78.0 470 2 C70641	9 78.0 3649 1 S18268	7 74.0 92 2 I70113	7 74.0 107 2 A72701 7 74.0 123 2 D72579	7 74.0 137 2	74.0 237 2 D40595	7 74.0 256 1 ASLJH2 7 74.0 340 2 A24026	7 74.0 401 2 T32737	7 74.0 429 1 FOLUGH	7 74 0 429 2 SO6073	7 74.0 513 2 887484	74.0 1385 2 H88569 7 74.0 1409 2 S41028	7 74.0 1466 2 T17138 CLIAA prote:
in the property of the propert	Copyrigh	ein sear	н	-10-009 HPRPPRG	~ .	83366 s	ts sati	ength: 0 ength: 20	Minimum Maximum Listing	PIR 78:* : pir1: : pir2: : pir3:	is the er tha ived by	ojo		0.00	000	88.0	0.0	0	0.0	0	0.0	0	00	0.0	00	0.0		. 0.	0.0	. 0 .	00	0.
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latrophilin-1, bra CLIBA protein - ra latrophilin-1, bra	CL1AB protein - ra CL1BB protein - ra cysteine proteinas	oryzacystatin II - hypothetical prote hypothetical prote	protein F3F9.20 [i cholecystokinin B conserved hypothet	gastrin/cholecysto alpha-2B-adrenergi gastrin receptor - cholecystokinin B
T18411 T17149 T18413	T17145 T17156 S13027	A38375 AE2630 S75053	H96811 S48049 AC3162	A47430 I51883 JQ1614 A46195
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1467 1471 1472	1510 1515 106	107 167 264	302 381 444	4 4 4 4 4 4 4 4 7 8 0 0 0
74.0 74.0 74.0	74.0 74.0 72.0	72.0	72.0	72.0
37	37 36	9 9 9 3 3 3	9 9 9 9 9 9	9 9 9 9 7 7 7 7
3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	64 62 64 62	33.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	8 4 4 6 0 11	4 4 4 4 5 6 4 6

ALIGNMENTS

 RESULT 1 PIHUSC salivary proline-rich phosphoprotein precursor PRH2 [validated] - human N,Alternate names: salivary acidic proline-rich protein PRH2 N,COntains: peptide P-C (basic proline-rich peptide IB-8b); proline-rich phosphoprotein C,Species: Homo sapiens (man)
 C;Date: 31-Mar-1981 #sequence revision 12-Apr-1996 #text change 08-Dec-2000 C;Accession: A25372; A19803; B57868; A92277; A92254; A94425; A91954; S02564; S02563; JP R;Medda, N.; Kim, H.S.; Azen, E.A.; Smithies, O.
 J. B101. Unew. 260, 11245-11130, 1985 A;Title: Differential RNA splicing and post-translational cleavages in the human saliva A;Reference number: A92492; MUID:85289325; PMID:2993301
A;Molecule 1, 723,7 A;Rosiduce: 1-166 <mae> A;Cross-references: GB:K03202; NID:g190481; PIDN:AAA60183.1; PID:g190482</mae>
R.Schlesinger, D.H.; Hay, D.I. Int. J. Pept. Protein Res. 17, 34-41, 1981 A.Title: Primary structure of the active tryptic fragments of human and monkey salivary A.Reference number: A91757; MUID:81191179; PMID:7228490
 A;Accession: A19803 A;Molecule type: protein A;Residues: 17-46 <sch></sch>
R;Kim, H.S.; Maeda, N. J. Biol. Chem. 261, 6712-6718, 1986 A;Title: Structures of two HaeIII-type genes in the human salivary proline-rich protein A:Reference number: A57868: MUID:86196106: PMID:3009472
A;Accession: B57869 A;Molecule type: DNA A:Residine: 1-166 <ktm></ktm>
 A. Cross-references: GB: M13058; NID: 9190513; PIDN: AAA98808.1; PID: 9190514 R; Wong, R.S.C.; Bennick, A.
 J. Biol. Chem. 255, 5943-5948, 1980 A;Title: The primary structure of a salivary calcium-binding proline-rich phosphoprotei A;Reference number: A92277; MUID:80204368; PMID:7380845
 A; Accessor: A2277 A; Molecule type: protein
 A;kealques: 1/-19, N',11-166 <won> A;Note: the aminof-terminal 46 residues are involved with inhibiting hydroxyapatite form P:Word B S C : Hofmann T : Beanick b</won>
7,702) 7.3.0.7, 70.3.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0
A/Contents: protein A A/Accession: A92254
A;Molecule type: protein A;Residues: 17-19,'N',21-122 <wo2></wo2>
 <pre>A;Schleshiger, D.H.; Hay, D.I.; in Peptides: Structure and Biological Function (Proc. Sixth Amer. Peptide Symp.), Gross A;Title: Complete primary structure of a proline-rich phosphoprotein (PRP-4), a potent</pre>
 A;Reference number: A94425

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salivary proline-rich phosphoprotein precursor PRH1 (allele PIF) - human C;Species: Homo sapiens (man) c;Species: Homo sapiens (man) solute: 29-Aug-1999 (pate: 29-Aug-1997) #sequence revision 29-Aug-1987 #text change 20-Aug-1999 (pate: 29-Aug-1972; A57868; S02562; G38355; S06153; B27307 R$; Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O. 4, Biol. Chem. 260, 11123-11130, 1985 A;Title Differential RNA splicing and post-translational cleavages in the human saliva A;Reference number: A92492; MUID:85289325; PMID:2993301
                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: mRNA
A, Reddudes 1.1-66 <MAB>
A, Cross-references: GR 8K03203, NID: 9190483, PIDN: AAA60184.1; PID: 9190484
A, Cross-references of N. 12.6718, 1986
A, Rille: Structures of two HaeIII-type genes in the human salivary proline-rich protein A, Reference number: A57868, MUID: 86196106; PMID: 3009472
A, Andecession: A57868
A, Molecule type: DNA
A, Residues: 1-166 <KIM>
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R;Hay, D.I.; Bennick, A.; Schlesinger, D.H.; Minaguchi, K.; Madapallimattam, G.; Schluc Babchem, T. 255, 15-21, 1988
A;Title: The primary structures of six human salivary acidic proline-rich proteins (PRP A;Reference number: S02562; MUID:89061650; PMID:3196309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A,Residues: 47-71 <HAY>
R,Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Blochemistry 30, 3351-3356, 1991
A,Title: Basic proline-rich proteins from human parotid saliva: relationships of the co
A,Reference number: A38355; MUID:91190884; PMID:1849422
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A,Residues: 123-166 «KAU»
R,Robinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
Biocham J. 263, 497-503, 1989
A,Title: Primary structure and possible origin of the non-glycosylated basic proline-ri
A;Reference number: S06153; MUID:90088384; PMID:2688632
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A,Residues: 123-166 <ROB>
R,Azen, B.A.; Kim, H.S.; Goodman, P.; Flynn, S.; Maeda, N.
A,Azen, E.H., Hu, Genet. 41, 1035-1047, 1987
A,Title: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich pr
A,Reference number: A27307; MUID:88074309; PMID:3687941
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proline-rich phosphoprotein precursor PRH1 (allele PIF) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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N;Alternate names: salivary acidic proline-rich protein
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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A; Cross-references: EMBL: K03203
C; Genetics: PRB: FMBL: K03203
A; Gene: GDB: PRH:
A; Cross-references: GDB: 119515; CMIM: 168730
A; Map position: 12p13.2-12p13.2
A; Introns: 22/1; 34/1
C; Superiamly: proline-ric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: proline-rich protein Keywords: phosphoprotein; saliva; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. ...
'... 0; Mismatches
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Les 8, Conservative
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                                       A/Molecule type: protein
A/Residues: 17-122 <8C2>
A/Note: the authors call this protein PRP-4
B/Sesidues: 17-12 <8C2>
A/Note: the authors call this protein PRP-4
B/Sechem. 87, 1071-1077, 1980
J. Biochem. 87, 1071-1077, 1980
A/Title: The amino acid sequence of a salivary proline-rich peptide, P-C, and its relating A/Secretion: Ap1554
A/Accession: Ap1554
A/Accession: Ap1554
A/Accession: Ap1554
A/Accession: Ap1554
A/Accession: Ap1564
A/Accession: A/Accession: Ap1564
A/Accession: A
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C'Superfamily: proline-rich protein
C'Superfamily: proline-rich protein
C'Superfamily: poline-rich prosphorotein; pyroglutamic acid; saliva
C'SEYWOOTGS: calcium binding; phosphorotein caperimental cape.
Fil-166/Domain: signal sequence #status experimental cape.
Fil-122/Product: protein A #status experimental cape.
Fil-146/Region: apartic mineral binding
Fil-147/Region: apartic mineral binding
Fil-17-166/Product: peptide F-C #status experimental cape.
Fil-17/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment F;24,38/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Accession: 802564
//Molecule type: protein
//Accession: 802563
//Accession: 80563
//Accession: 80563
//Accession: 80563
//Accession: 900106; MUID:86222916; PMID:3710693
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Myoleule type: protein
A;Residues: 123-166 «KAU»
R;Residues: 123-166 «KAU»
R;Robinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
Biochem. J. 263, 497-503, 1989
A;Title: Primary structure and possible origin of the non-glycosylated basic proline-ric
A;Reference number: 806153; MUID:90088384; PMID:2688632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Molecule type: protein
;Residues: 17-161,'Q',163-166 <SC3>
;Rasidues: 17-161,'Q', 163-166 <SC3>
;Rasidues: 17-161,'Q', 163-166 <SC3>
;Rayerimental source: paroid gland
;Ratifman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
;Chemistry 30, 3351-3356, 1991
;Ratiference proline-rich proteins from human parotid saliva: relationships of the cov
;Ratiference number: A38355; MUID:91190884; PMID:1849422
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;Comment: The proposed biological functions are a highly potent inhibitor of crystal
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0; Mismatches

8; Conservative

Matches

Local Similarity

Query Match

117 HPRPPRGR 124

g

RESULT B25372

1 HPRPPRGR

100.0%; 100.0%;

A,Cross-references: GDB:119516; OMIM:168790 A,Map position: 12p13.2-12p13.2 A;Introns: 22/1; 34/1

Gene: GDB: PRH2

A;Molecule type: protein A;Residues: 123-166 <ROB>

Accession: S06153

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C;Species: Mus musculus (house mouse)
C;Accession: A54741; 148901
R;Korsgren, C; Cohen, C:M.
Genomics 21, 478-485, 1994
A;Title: CDNA sequence_revision 18-Aug-1995 #text_change 05-Nov-1999
C;Accession: A54741; MUD:95048323; PMID:7959722
A;Accession: A54741
A;Reference number: A54741; MUD:95048323; PMID:7959722
A;Accession: A54741
A;Accession: A7401
A;Acce
    C;Comment: This enzyme catalyzes both de novo synthesis and chain elongation of fatty; C;Genetics:
A;Genetics:
C;Genetics:
C;Superfamily:
C;Superfamily:
C;Superfamily:
C;Keywords: acyltransferase; coenzyme A; phosphopantetheine; phosphoprotein
F;2188-2193/Region: nucleotide binding #status predicted
F;57Active site: Ser #status predicted
F;693/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
F;2598/Active site: Cys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rikawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch DNA Res. S, S5-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A; Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Pyrococcus horikoshii
.Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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C,Superfamily: Pyrococcus horikoshii hypothetical protein PH0192
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2796;
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85.7%; Pred. No. 13;
live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.0%; Score 41, DB 2, I
Best Local Similarity 87.5%; Pred. No. 1.88+02;
Matches 7; Conservative 0; Mismatches 1,
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A,Molecule type: mRNA
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Best Local S:
Matches 6,
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C.Species: Mycobacterium bovis
R.Fernandes, N.D.; Kolattukudy, P.E.
A.Fernandes, N.D.; Kolattukudy, P.E.
A.Title: Cloning, sequencing and characterization of a fatty acid synthase-encoding gene
A.Title: Cloning, sequencing and characterization of a fatty acid synthase-encoding gene
A.Accession: JC4743; MUID:96200863; PMID:8621098
A.Accession: JC4743
A.Accession: JC4743
A.Accession: JC4743
A.Accession: Mycobacterium tuberculosis var. bovis BCG
A.Coss-references: GB:U36763; NID:g1036834; PIDN:AAB03809:1; PID:g1036835
A.Note: the source is designated as Mycobacterium tuberculosis var. bovis BCG
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R. Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Parkhill, T.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Decipharing the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; Muideic acid sequence not shown; translation not shown
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C;Genetics:
A;Gene: Rv1215c
                                                              R. Azen, E.A.; Kim, H.S.; Goodman, P.; Flynn, S.; Maeda, N. Am. J. Hum. Genet. 41, 1035-1047, 1987
A,Title: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich A,Reference number: A27307; WUID:88074309; PMID:3687941
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C,Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 29-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Rv1215c - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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Pred. No. 0
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                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 12p13.2-12p13.2
C;Superfamily: proline-rich protein
C;Keywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                            A;Residues: î-171 <AZE>
A;Cross-references: EMBL:K03203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 HPRPPRGR 129
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534 YPRPPRGR 541
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85.78;

Query Match Best Local Similarity

Best Loc Matches

6; Conservative

350 HPRPPNG 356

1 HPRPPRG 7

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hypothetical protein Rv0696 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Unl-1998 #sequence_revision 17-Unl-1998 #text_change 22-Oct-1999
C;Accession: C70641
R;Oole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-S44, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:9825987; PMID:9634230
A;Accession: C70641
A;Scatues preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-470 < COL.
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A; Residues: 224-940;1319-2010,2373-3307 <CCQ>
A; Residues: 224-940;1319-2010,2373-3307 <CCQ>
A; Cross-references: EMBL:X57310
A; Note: the source is designated as Nocardia lactamdurans
R; Coque, J.J.R.; Liras, P.; Laiz, L.; Martin, J.F.
J. Bacteriol. 173, 6258-6264, 1991
A; Title: A gene encoding lysine 6-aminotransferase, which forms the beta-lactam precurs
A; Reference number: A38171; MUID:92011390; PMID:1917857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c, cearer. Proceed to the second of the seco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase - Streptomyces lactamdurans C;Species: Streptomyces lactamdurans C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Nov-2000 C;Accession: S18268; S15283; B38171
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A,Reaidues: 1-3649 <MAR>
A,Reaidues: 1-3649 <MAR>
A,Reaidues: 1-3649 <MAR>
A,Cross-references: EMBL:X57310; NID:g45005; PIDN:CAA40561.1; PID:g45006
B,Coque, U.T.R.; Martin, U.F.; Calzada, U.G.; Liras, P.
Mol. Microbiol: 5, 1125-1133, 1991
A,Title: The cephamycrin biosynthetic genes pcbAB, encoding a large multidomain peptide genes in Acremonium chrysogenum and Penicillium chrysogenum.
A,Reference number: S15283; MUID:92065808; PMID:1956290
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85.7%; Pred. No. 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Status: nucleic acid sequence not shown
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Best Local Similarity 85.7
Matches 6; Conservative
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A,Moleoule type: DNA
Residues: 1-23 <CO2>
A,Cross-references: GB:S57006
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A, Accession: S18268
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A;Cross-references: GB:UZ0824; NID:g695172; PIDN:AAC13802.1; PID:g695187
A;Note: the nucleotide seguence was submitted to the EMBL Data Library, February 1995
                                          A,Residues: 1-352,'A',354-620,'S',622-691 <RES>
A;Cross-references: EMBL:U03487; NID:G424119; PIDN:AAA62275.1; PID:G424120
C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Keywords: blocked amino end; lipoprotein; myristylation
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
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C;Species: equine herpesvirus 2
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S55609
M:Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MuID:95302501; PMID:7783207
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C,Species: Mesocricetus auratus (golden hamster)
C,Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C,Accession: 146185
R;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, W.J.; German, M.S.
R;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, 1994
A;Title: Pancreatic beta cells express a diverse set of homeobox genes.
A;Reference number: 148185; MUID:95083670; PMID:7991607
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A, Cross-references: EMBL:X81403; NID:9587455; PIDN:CAA57161.1; PID:9587456
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C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;157-213/Domain: homeobox homology <HOX>
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Pred. No. 66;
0; Mismatches 1; Indels
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Pred. No. 49;
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PKPPRGR 19

PRPPRGR 8

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78.0%; 85.7%;

Query Match Best Local Similarity

6; Conservative

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42

RESULT 10 C70641

1 HPRPPRG 7

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Gaps

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Score 37; DB 2; Length 107; Pred. No. 33; 1; Mismatches 1; Indels

74.0%;

us-10-009-709-9.rpr

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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: A72701
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Takamiya, M.; Mauda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jamazaki, J.; DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                A,Molecule type: DNA'
A,Residues: 1-107 «KAW»
A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA80009.1; PID:d1043795; PID:g51
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1024
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Best Local Similarity 75.0°
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AB3238
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 0.2-011-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jun-2000
C;Accession: 170113
R;Craft, C.M.; Whitmore, D.H.; Wiechmann, A.F.
J. Biol. Chem. 269, 4613-4619, 1994
A;Title: Cone arrestin identified by targeting expression of a functional family. A;Reference number: 155423; MUID:94140898; PMID:8308033
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A;Molecule type: DNA
A;Residues: 1-450 «KUR»
A;Cross-references: GB:AE008690; PIDN:AAL46320.1; PID:g17744106; GSPDB:GN00189
A;Experimental source: strain C58 (Dupont)
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A;Molecule type: m2NA
A;Molecule type: m2NA
A;Residues: 1-92 < RES5.
A;Cross-references: EMBL:U03628; NID:g458204; PIDN:AAA17552.1; PID:g458205
C;Superfamily: arrestin
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                                78.0%; Score 39; DB 1; Length 3649; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels
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A;Gens. Atu6084
Genome: plasmid
C;Superfamily: nitrilotriacetate monooxygenase
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Matches 6; Conservative
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A72701 hypothetical protein APE1024 - Aeropyrum pernix (strain K1)

RESULT 14

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Appotherical protein APE1916 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999
#sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D72579
R;Kawarabayasi, Y:, Hino, Y:, Horikawa, H:, Yamazaki, S.; Haikawa, Y:, Jin-no, K.; Takawa, H:, Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y:, Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Reference number: A72450; MUID:99310339; PMID:10362966
A;Accession: D72579
A;Reference number: A72450; MUID:99310339; PMID:10362966
A;Accession: D72579
A;Residues: Drallminary
A;Residues: 1-123 cKAW>
A;Cross-references: DDA:APD00062; NID:95105244; PIDN:BAAB0921.1; PID:d1044707; PID:g51
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1916
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Copyright (c) 1993 - 2004 Compugen Ltd.
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GAG_HTL1A
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ALIGNMENTS

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VARIANT PRH2-3 LYS-163
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SEQUENCE FROM N.A.

TISSUE=Neuroblastoma;

MEDLINE=21665991; PubMed=11807986;

MIMMER K., Zhu X.-X., Rouillard J.M., Ambros P.F., Lamb B.J.,

Midck R., Eckart M., Weinhausl A., Fonatsch C., Hanash S.M.;

Kuick R., Eckart M., Weinhausl A., Fonatsch C., Hanash S.M.;

T. "Combined restriction landmark genomic scanning and virtual genome scans identify a novel human homeobox gene, ALX3, that is hypermethylated in neuroblastoma.";

T. Genes Chromosomes Cancer 33:285-294(2002).

C. - FUNCTION: Transcriptional regulator with a possible role in patterning of mesoderm during development (By similarity).

C. -- SUNCELLULAR LOCATION: Nuclear (By similarity).

C. -- SUNILARITY: Belongs to the paired homeobox family.

C. -- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALX3 HUMAN STANDARD; PRT; 343 AA.
095076; 095075;
16-0CT-2001 [Rel. 40, Created)
16-0CT-2001 [Rel. 40, Last sequence update)
18-FEB-2003 [Rel. 41, Last annotation update)
Homeobox protein aristaless-like 3 (Proline-rich transcription factor
                                     PHOSPHOPROTEIN 1/2.
SALIVARY ACIDIC PROLINE-RICH
PHOSPHOPROTEIN 3/4.
PEPTIDE P-C.
INHIBIT HYDROXYAPATITE FORMATION, BIND
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 50; DB 1; Length 166; 100.0%; Pred. No. 0.19;
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                      SALIVARY ACIDIC PROLINE-RICH
                                                                                                                                                                                                      PHOSPHORYLATION.
D -> N (in allele PRH1-4).
FTIG=VAR. 005563.
D -> N (in allele PRH2-1).
FTIG=VAR. 005564.
G -> K (in allele PRH2-3).
FTIG=VAR. 005565.
                                                                                                                                                                                                                                                                                                                                                 F -> P (IN REF. 10).
A7DF62BF94E3C3EF CRC64;
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Matches 8; Conservative
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MIM; 606014; -.
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ALX3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 17-122 (PROTEIN A).
Schlesinger D.H., Hay D.I.;
"Complete primary structure of a proline-rich phosphoprotein (PRP-4),
a potent inhibitor of calcium phosphate precipitation in human parotid
saliva.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: Secreted.
-:- PTM: Proteolytically cleaved; PRP-2, FRP-1, and PIF-S yield PRP-4, PRP-3 (protein A), and PIF-F, respectively.
-:- POLYMORPHISM: Allele PRH1-4 is also known as PRH1 DA allele; allele PRH2-1 is also known as PR1 or protein C; allele PRH2-3 is also known as PR1.
                                                                                                                                                                                                                            [8]
SEQUENCE OF 17-122 (PROTEIN A).
SEQUENCE OF 17-122 (PROTEIN A).
MEDLINE-79173237; PubMed-438215;
MODR R.S.C., Hofmann T., Bennick A.;
"The complete primary structure of a proline-rich phosphoprotein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 123-166 (PEPTIDE P-C).
MEDLINE-80227634; PubMed=7390979;
ISemura S., Saitoh E., Sanada K.;
"The amino acid sequence of a salivary proline-rich peptide, P-C, and its relation to a salivary proline-rich phosphoprotein, protein C.";
J. Biochem. 87:1071-1077 (1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (In) Gross E., Meienhofer J. (eds.);
Peptides: structure and biological function (Proceedings of the 6th
American peptide symposium); pp.133-136, Pierce Chemical Co.,
Rockford II. (1979).
"The primary structure of a salivary calcium-binding proline-rich phosphoprotein (protein C), a possible precursor of a related
                                                                                                                  MEDILINE-81191179; PubMed=1728490; Schlesinger D.H., Hay D.I.; Prinesty Structure of the active tryptic fragments of human and monkey salivary anonic proline-rich proteins."; in. 7 Pept. Protein Res. 17:34-41(1981).
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GO; GO:006515; C:extracellular space; TAS.
Repat; Parotid gland; Phosphorylation; Signal; Polymorphism;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                      human saliva.";
J. Biol. Chem. 254:4800-4808(1979)
[9]
                                              salivary protein A.";
J. Biol. Chem. 255:5943-5948(1980)
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EMBL; K03203; AAA60184.1; --
EMBL; M13057; AAA980807.1; --
Genew; HGNC:9366; PRH1.
Genew; HGNC:9366; PRH2.
MIM; 168730; --
MIM; 168730; --
                                                                                                         SEQUENCE OF 17-46 (PROTEIN C)
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InterPro; IPR007104; Paired_homeo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mouse Alax: an aristaless-like homeobox gene expressed during embryogenesis in ectomesenchyme and lateral plate mesoderm.";
Dev. Biol. 199:11-25 (1998).

-!- FUNCTION: Transcriptional regulator with a possible role in patterning of mesoderm during development.
-!- SUBCELIUIAR LOCATION: Nuclear (By similarity).
-!- SUBCELIUIAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: Predominantly in neural crest-derived mesenchyme and in lateral plate mesoderm. Prominent expression in frontonasal head mesenchyme and in the first and second pharyngeal arches and some of their derivatives. High expression is also seen in the tail and in many derivatives of the lateral plate mesoderm in the tail and in many derivatives of the lateral plate mesoderm including the limbs, the body wall, and the genital tubercle.
-!- DEVELOPMENTAL STAGE: Expressed in embryos from 8 days of gestation
                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein aristaless-like 3 (Proline-rich transcription factor
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                  ;
           InterPro; IPR007104; Paired homeo.
Pfam; PF00046; homeobox; 1.
SWART; SW00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS0017; HOMEOBOX 1; 1.
PROSITE; PS0017; HOMEOBOX 2; 1.
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ten Berge D., Brouwer A., el Bahi S., Guenet J.-L., Robert B., Meijlink P.,
                                                                                                                                                                                    Score 39; DB 1; Length 343;
Pred. No. 22;
0; Mismatches 1; Indels
                                                                                                                                 72 72 L -> M (IN REF. 1; AAD01417).
86 86 F -> L (IN REF. 1; AAD01417).
343 AA; 36904 MW; 17AFC7ECD40B942F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the paired homeobox family.
                                                                                                                                                                                                                                                                                                                                      343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                     HOMEOBOX
                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NIH Swiss;
MEDLINE=98340878; PubMed=9676189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T03343; -.
MGD; MGI:1277097; Alx3.
InterPro; IPR001356; Homeobox.
 InterPro; IPR001356; Homeobox
                                                                                                                                                                                    h
Similarity 85.7%;
6; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U96109; AAC15094.1; -. HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                   39 HPAPPRG 45
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                           1 HPRPPRG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                     153
                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                 CONFLICT
                                                                                                                                                            SEQUENCE
                                                                                                                       DNA BIND
                                                                                                                                                                                                                                                                                                             T 3
MOUSE
                                                                                                                                                                                                                                                                                                                                      ALX3
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Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Makabe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Watsuo K., Nishikawa T., Kimura K., Yamashita H., Watsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Sugiyama A., Kawakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Nakamo CDM. Sequencing project.";
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOId=08TF68-2; Sequence=VSP 006920; SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2384 HUMAN STANDARD; PRT; 576 AA.
QBTF68; 015407; QBN938;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 384 (Nuclear matrix transcription factor 4)
(CAG repeat protein 1).
ZNF384 OR NMP4 OR CAGHI.
                                                                                                                                                                                                                                                                                                               ..
0
                                                              PROSTIE; PS00027; HOMEOBOX 1; 1.
PROSTIE; PS00071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
DNA BIND 153
ERQÜENCE 343 AA; 36850 MW; 87900BF977FACD2D CRC64;
                                                                                                                                                                                                                                                         78.0%; Score 39; DB 1; Length 343; 85.7%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q8TF68-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2).
Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM0389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 395-576 FROM N.A.
                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 85...
Fra 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     39 HPAPPRG 45
                                                                                                                                                                                                                                                                                                                                                                 1 HPRPPRG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsuo M.Y.;
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us-10-009-709-9.rsp

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579 AA;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                Name=1;
                                                                                                                                                                                                                                                                                                   Name=3
                                                                                                                                                                                                                                                                 Name=2
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CONFLICT
SEQUENCE
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Anodified and til.

Entities requires a or send an email to lice.

ENEL, 48707028; BAB8125.1; -

EMBL; 48707038; BAB8125.1; -

EMBL; 4807038; BAB8125.1; -

EMBL; 4807038; AAB91437.1; -

EMBL; 48070609; Zaf C2H2; B.

DR PRODOM; PROTOMORY Zaf C2H2.

DR PROSTE; PROTOMORY Zaf C2H2.

NA PING 228 C
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MEDIATE=2013645; PubMed=10669742;
MEDIATE=2013645; PubMed=10669742;
Makamoto T., Yamagata T., Sakai R., Ogawa S., Honda H., Ueno H.,
Hirano N., Yazaki Y., Hirai H.;
Hirano N., Yazaki Y., Hirai H.;
"CIZ, a zinc finger protein that interacts with pl30cas and activates
"CIZ, a zinc finger protein metalloproteinases.";
Mol. Cell. Biol. 20:1649-1658(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1), SUBCELLULAR LOCATION, DNA-BINDING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STEAIN=Sprague-Dawley;
MEDLINE=21024193; PubMed=11149472;
Thunyakitpisal P., Alvarez M., Tokunaga K., Onyia J.E., Hock J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EQJ4; Q9EQJ2; Q9EQJ3; Q9JMJ5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 384 (Nuclear matrix transcription factor 4)
(Cas-associated zinc finger protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
-!- SIMILARITY: Contains 8 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 85.7%; Pre Matches 6; Conservative 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 PKPPRGR 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z384 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
Z384_RAT
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KI "Cloning and functional analysis of a family of nuclear matrix ranscription factors (NP/NMP4) that regulate type I collagen Expression in osteoblasts."

RI J Bone Miner. Res. 16:10-23(2001).

C. -! FUNCTION: Transcription factor that binds the consensus DNA CC NMP1. MMP3 mMP7 and COLIA!.

-! SUBJUNT: Interacts with Cas.

C. -! SUBJUNT: Interacts with Cas.

C. -! SUBJUNT: Interacts with Cas.

C. -! ALTERNATIVE PRODUCTS:

Event-alternative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=Q9EQJ4-3; Sequence=VSP 006922; TISSUE SPECIFICITY: Expressed in osteocytes, osteoblasts, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chondrocytes in bone.
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FBC242E0D1050C45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9EQJ4-2; Sequence=VSP_006921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isold=Q9EQJ4-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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us-10-009-709-9.rsp

189 PKPPRGR 195

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2 PRPPRGR

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MM24 MOUSE STANDARD, PRT, 618 AA.

09R052; 092007.

16-0072-2001 (Rel. 40, Last sequence update)

16-0072-2001 (Rel. 41, Last annotation update)

28-FEB-2003 (Rel. 41, Last annotation update)

48-FEB-2003 (Rel. 41, Last annotation update)

(Membrane-type matrix metalloproteinase-24 precursor (EC 3.4.24.-) (MMP-24)

(Membrane-type matrix metalloproteinase 5) (MT-MMP 5) (Membrane-type-5

MMP24 OR MTSMMP OR MMP21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-20086420; PubMed=10622708;
Wang X., Yi J., Lei J., Pei D.Q.;
Wang X., Yi J., Lei J., Pei D.Q.;
Expression, Purification and characterization of recombinant mouse
NTS-MMP protein products.";
FEBS Lett. 462:261-266(1999).
-! FUNCTION: Activates progelatinase A. May also be a proteoglycanse
involved in degradation of proteoglycans, such as dermatan sulfate
and chondroitin sulfate proteoglycans. Cleaves partially
fibronectin, but not collagen type I, nor laminin.
-! COPACTOR: Binds I zinc ion per subunit, calcium (By similarity).
-! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN ALSO SHED FROM CELL
SURFACE AS SOLUBLE PROTEINASE, BY A PROTEOLYTIC CLEAVAGE.
-! TISSUE SPECIFICITY: Expressed in brain. Expressed at low level in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterization of the fifth membrane-type matrix
                                                                                                                                                                                                                                                                                                                                  Selfu M.; "Identification of a new membrane-type matrix metalloproteinase, MTS-MMP, that is expressed predominantly in cereballum."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: Expressed at day 11 until day 15, before dropping around day 17 before birth.

PTM: The precursor is cleaved by a furin endopeptidase (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similaritŷ).
SIMILARITY: Belongs to peptidase family MIOA.
SIMILARITY: Contains 1 hemopexin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND MUTAGENESIS OF GLU-256. STRAIN=BALB/c; TISSUB=Brain; MEDLINE=99185121; PubMed=10085137; Pi O.; I dentification and characterization of the fif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; MIO.023; ...
MGD; MGI.1341867; Mmp24.
InterPro; IPR000585; Hemopexin.
InterPro; IPR001818; Pept MIOA MI2B.
InterPro; IPR006025; Pept_M_Zn_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metalloproteinase MT5-MMP.";
J. Biol. Chem. 274:8925-8932(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB021226; BAA82966.1; -. EMBL; AJ010262; CAA09055.1; -. HSSP; P03956; 1CGL.
                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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GRAAPOGASRWSGWRAPGRLLP -> AALRRARPRAGALAG
FGAAA (IN REF. 2)
KFTGADA -> SRFOR (IN REF. 2).
LEP -> SGA (IN REF. 2).
R -> K (IN REF. 2).
PPLGD -> RPWG (IN REF. 2).
I -> KP (IN REF. 2).
I -> KP (IN REF. 2).
I -> L (IN REF. 2).
I -> L (IN REF. 2).
L -> R N REF. 2).
L -> R N REF. 2).
WW; 62C0086BlE54Bl06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                         (BY SIMILARITY).
                                                                                                                                                                                                                                                              (BY SIMILARITY)
(BY SIMILARITY)
          Pfam; PF00045; hemopexin; 4.

Pfam; PF00045; hemopexin; 4.

Pfam; PF00043; Peptidase M10; 1.

Pfam; PF0393; Peptidase M10; 1.

PROSITE; PR00138; MATRIXIN.

SMART; SM00129; HX; 4.

SMART; SM00215; ZMC; 1.

PROSITE; PS00024; HEMOPEXIN; 1.

PROSITE; PS00024; HEMOPEXIN; 1.

Hydrolase; Metalloprotease; 2inc; Calcium; Signal; Zymogen; Transmembrane; Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 78.0%; Score 39; DB 1; Length 618; Best Local Similarity 100.0%; Pred. No. 41; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                    BY SIMILARITY.
MATRIX METALLOPROTEINASE-24.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                          CYSTEINE SWITCH (POTENTIAL)
ZINC (CATALYTIC) (BY SIMILA
                                                                                                                                                                                       POTENTIAL,
CYTOPLASMIC (POTENTIAL),
HEMOPEXIN-LIKE,
                                                                                                                                                                                                                                                              (CATALYTIC)
(CATALYTIC)
                                                                                                                                                                                                                                                                                    BY SIMILARITY.
POLY-ARG.
                                                                                                                                                                                                                                                             ZINC
InterPro; IPR006026; Peptidase_M.
                                                                                                                                                                                                                                                                                                                                                                                                                  70490 MW;
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502
589
618 AA;
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase
(RC 6.3.2.26) (Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase) (ACV synthetase) (ACVS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                    PRT; 3649 AA
                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nocardia lactamdurans.
                                               ACVS NOCLA
ACVS NOCLA
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us-10-009-709-9.rsp

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SEQUENCE FROM N.A.
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
   SOLUTION SOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                   -!- CATALYTIC ACTIVITY: L-2-aminohexanedioate + L-cysteine + L-valine + 3 ATP = N-[L-5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine + 3 AMP + 3 diphosphate.
-!- COFACTOR : Contains 3 covalently bound phosphopantetheines.
-!- PATHWAY: Biosynthesis of penicillin and cephalosporin; first step.
-!- PATHWAY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
20-Ichol-Phosphate mannosyltransferase (EC 2.4.1.83) (Dolichol-phosphate mannose synthase) (Dolichyl-phosphate beta-D-mannose synthase) (Mannose-P-dolichol synthase) (MPD synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      820 PHOSPHOPANTETHEINE (BY SIMILARITY)
1896 PHOSPHOPANTETHEINE (BY SIMILARITY)
2944 PHOSPHOPANTETHEINE (BY SIMILARITY)
3502 THIOBETERASE (BY SIMILARITY)
AA; 404079 MW; 6FD095704F85BE6B CRC64;
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DOMAIN 2 (CYSTEINE-ACTIVATING).
DOMAIN 3 (VALINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 3.
formed through the participation of amino acid thiolester
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Pred. No. 2.6e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 3 acyl carrier domains.
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100.0%; Pre
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HSSP; P14687; 1AMU.
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE
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DOMAIN
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DPM1 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rawai J., Shinagawa A., Shibata X., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata X., Yoshino M., Itoh M., Ishii Y., Rawai T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Rakawa T., Izawa K., Izawa M., Nishii K., Kiyosawa H., Kosukawa T., Samanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Reischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Rubil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Barkei M., Dult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Austincich S., Hill D., Hofmann M., Mazzarelli J., Mombaerts P., Austincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Ayanafizaki Y., Kawaji H., Kohtsuki S., Andaraki Z., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is the mannosyl donor in pathways leading to N-glycosylation,
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                        Tomita S., Inoue N., Maeda Y., Ohishi K., Takeda J., Kinoshita T.; "A homologue of Saccharomyces cerevisiae Dpmlp is not sufficient for synthesis of dolichol-phosphate-mannose in mammalian cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                     STEAIN=C57BL/6J; IISSUE=Cerebellum, Lung, and Small intestine; MEDLINE=21085660; PubMed=11217851;
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Pred. No. 24;
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                                                                                                                                                                                                                         J. Biol. Chem. 273:9249-9254 (1998)
MEDLINE=98204925; PubMed=9535917;
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EMBL, AKO05268; BAB23920.1; -.
EMBL, AKO04834; BAB2362.1; -.
EMBL, AKO04849; BAB25735.1; -.
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Best Local Similarity 85.7%;
Matches 6; Conservative
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61 HPKPPHG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUL, Scocca J.R., Walker B.K., Wu J.S., Krag S.S.;
Pul., Scocca J.R., Walker B.K., Wu J.S., Krag S.S.;
T. Mandation in B4-2-1 GHO cells defective in MpD synthase activity.";
T. Mandation in B4-2-1 GHO cells defective in MpD synthases.
T. Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
T. FUNCTION: Transfers mannose from GDP-mannose to Golichol
monophosphate to form dolichol phosphate mannose (Dol.P-Man) which
T. Stycosyl phosphatidylinositol membrane anchoring, and O-
mannosylation of proteins (By similarity).
T. CAPALKITC ACTIVITY: GDP-mannose + dolichyl phosphate = GDP +
dolichyl D-mannosyl phosphate.
T. CAPALKITON: Endoplasmic reticulum (By similarity).
T. SIMILARITY: Belongs to the glycosyltransferase family 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                  28-FEE-2003 (Rel. 41, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
28-FEE-2003 (Rel. 41, Last annotation update)
Dolichol-phosphate mannosyltransferase (EC 2.4.1.83) (Dolichol-phosphate mannose synthase) (Dolichyl-phosphate beta-D-mannose (Mannose-P-dolichol synthase) (MpD synthase)
                                                                                                                                                            Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.0%; Score 38; DB 1; Length 266; 85.7%; Pred. No. 25; 1: Mismatches 0; Indels
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Pfam; PF00535; Glycos transf 2; Ī.
Transferase; Glycosyltransferase; Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29654 MW; 4AFB37EA3AC3329D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-ZUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Arrestin-C (Cone arrestin) (Fragment).
                            266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley; TISSUE=Pineal gland;
MEDLINE=94140898; PubMed=8308033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF121895; AAD30975.1; -.
                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                 NCBI_TaxID=10029;
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                         DPM1 CRIGR
Q9WUB3;
                                                                                                                                     synthase).
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RESULT 9
DPM1_CRIGR
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                                                                    family.";
J. Balol. Chem. 269:4613-4619(1994).
-!- FUNCTION: May play a role in an as yet undefined retina-specific
signal transduction. Could binds to photoactivated-phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birch A., Leiser A., Robinson J.A.; "Cloning, sequencing, and expression of the gene encoding methylmalonyl-coenzyme A mutase from Streptomyces cinnamonensis."; J. Bacteriol. 175:3511-3519(1993).
Craft C.M., Whitmore D.H., Wiechmann A.F.; "Cone arrestin identified by targeting expression of a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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Streptomycineae, Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L10064; AAA03039.1; -.
PIR; D40595; D40595.
PYPothetical protein.
SEQUENCE 237 AA; 25025 MW; D9C55FED795A8455 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-0CT-2010 (Rel. 40, Last annotation update)
Hypothetical 25.0 kba protein in mutA 5'region (ORF-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 92 AA; 9878 MW; 88F0C948643C83B9 CRC64;
                                                                                                                                                                                                                     red/green opsins.
-!- TISSUE SPECIFICITY: Retina and pineal gland.
-!- SIMILARITY: Belongs to the arrestin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.0%; Score 37; DB 1; 71.4%; Pred. No. 12; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; PO8168; ICFI.
InterPro; IPR000698; Arrestin.
InterPro; IPR000699; Arrestin.
Pfam; PF02752; arrestin C; 1.
ProDom; PD002099; Arrestin; 1.
PROSITE; PS00295; ARRESTINS; PARTIAL.
Sensory transduction; Vision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A3823.5;
MEDLINE=93273720; PubMed=8099072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U03628; AAA17552.1; -. PIR; I70113; I70113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces cinnamonensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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Tue Apr

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88039140; PubMed-3118220;
Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Leccog J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating activities. It seems to down-regulate the CD4(T4) antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, N. S05291, CALL.

PIRI, D26262, ASLJH2.

R HIV, M15390, NEF$2R0D.

R InterPro; IPR001558; HIV Nef.

DR Pfaus, PF004691; Proteini, 1.

DR Probom, PR000031; HIV Nef; J.

Namiriacupi glyprotein.

PHOSPHORYLATION; Lipoprotein.

PHOSPHORYLATION (BY PKC).

PHOSPHORYLATION (BY PKC).

ON TOTAL (MW, 55BAIB78E7ICCA85 CRC64;

Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 2 (isolate ROD) (HIV-2). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 74.0%; Score 37; DB 1; Length 256; Local Similarity 85.7%; Pred. No. 34; les 6; Conservative 0; Mismatches 1; Indels
Length 237;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=87173056; PubMed=3031510;
Guyader M., Emerman M., Sonigo P., Clavel F., Montagnier
                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome organization and transactivation of the human immunodeficiency virus type 2."; Nature 326:662-669(1987).
                                                                                                                                                                                                                                                                           Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
74.0%; Score 37; DB 1;
100.0%; Pred. No. 32;
ive 0; Mismatches 0
                                                                                                                                                                                                                         13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                        256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
 Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 330:266-269(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 HSRPPRG 15
                                                                                                    113 PRPPRG 118
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                                                                   2 PRPPRG 7
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ERMA_ARTS3
ID _ERMA_ARTS3
AC P09891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an oncogene
                                                                                                                                                       RESULT 12
NEF HV2RO
ID NEF HV2RO
AC P04600;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Alizon M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + rRNA = S-adenosyl-L-homocysteine + rRNA containing N(6)-methyladenine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 35:259-270(1985).
-!- PUNCTION: THIS PROTEIN PRODUCES A DIMETHYLATION OF THE ADENINE
-!- PROSTIDIE AT POSITION 2.058 IN 2.15 RRMA, REGULTING IN REDUCED
AFFINITY BETWEEN RIBOSOMES & MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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21-UUL-1986 (Rel. 01, Last sequence update)
21-UUL-1986 (Rel. 42, Last amotation update)
GAG polyprotein [Contains: Major core proteins P19 and P24; Nucleic acid-binding protein P15].
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=66006275; PubMed=4043733;
ROBERTS A.N., Hudson G.S., Brenner S.;
ROBERTS A.N., Hudson G.S., Brenner S.;
"An erythromycin-resistance gene from an erythromycin-producing strain of Arthrobacter sp.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
11-OCT-2003 (Rel. 42, Last amnotation update)
11-MAR-1884 adenine N-6-methyltransferase (EC 2.1.1.48) (Macrolide-lincosamide-streptogramin B resistance protein) (Erythromycin
                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Propionibacterineae; Nocardioidaceae; Aeromicrobium.
NCBI_TaxID=31956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 1; Length 340;
Pred. No. 46;
0; Mismatches 0; Indels
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Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBI_TaxID=11926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M11276; AAA22075.1; -..
InterPro; IPR001737; RRNA A dimeth.
InterPro; IPR001051; SAM Dind.
InterPro; IPR001051; SAM Dind.
SMART; SW00650; RADC; 1.
SWART; SW00650; RADC; 1.
PROSTITE; PS01131; RRNA A DIMETH; 1.
AALIBIOCI CRESSEAGNCE; TRANSFERASE; METHYLERANSFERASE.
SEQUENCE 340 AA; 37453 MW; E99A714C391952B5 CRC64;
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100.0%; Pre
                                                                                                                                                                                                                                         (strain B3381).
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Best Local Similarity 100...
6; Conservative
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                                                                                                                                                                           resistance protein)
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                                                                                                                                                                                                                                         Arthrobacter sp.
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Viruses; Retroid viruses; Retroviridae; Deltaretrovirus
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; JOC29; AAA-.

EMBL; JOC30; AAA-.

EMBL; JOC30; AAA-.

EMBL; JOC30; AAA-.

EMBL; JOC30; Gag_D19.

A InterPro; IPR008916; Retrov_capsid_C.

EN InterPro; IPR008916; Retrov_capsid_N.

EN InterPro; IPR001899; Znf CCHC.

Exam; PF0228; Gag_D19; I.

Exam; PF00560; Gag_D24; I.

Exam; FF00560; Gag_D269; Gag_D269; I.

Exam; FF00560; Gag_D269; I.

Exam; FF00660; I.

Exam; FF
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01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Major core proteins P19 and P24; Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structural protein p15 ";

BESS Lett. 162:390-395 (193).
-!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
-!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
[2]
SEQUENCE OF 131-155.
SEQUENCE OF 131-155.
OFFICIAL SEQUENCE SEQUENCE OFFICE SEQUENCE SEQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=84029174; PubMed=6313426;
Copeland T.D., Oroszlan S., Kalyanaraman V.S., Sarngadharan M.G.,
Gallo R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human T-cell leukemia virus type I (Caribbean isolate) (HTLV-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Complete amino acid sequence of human T-cell leukemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.0%; Score 37; DB 1; Length 429; 100.0%; Pred. No. 59; 0; Indels ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 6; Conservative
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GAG_HTL1C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                         MEDINE-8874338; PubMed=2899128;
Malik K.T.A., Even J., Karpas A.;
Molecular coloning and complete nucleotide sequence of an adult T
"Molecular coloning and complete nucleotide sequence of an adult T
call leukaemia virus/human T cell leukaemia virus type I
(ATLV/HTLV-I) isolate of Caribbean origin: relationship to other
members of the ATLV/HTLV-I subgroup.";
J. Gen. virol. 69:1695-1710(1988).
I. PRM: Specific enzymatic cleavages in vivo yield mature proteins.
I. SIMILARITY: Contains 2 CCHC-type zinc fingers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 429;
Pred. No. 59;
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INTERPO, IPRO03139; Gag_D19.
INTERPO; IPRO03139; Gag_D24.
INTERPO; IPRO080121; Gag_D29.
INTERPO; IPRO08016; Retrow_capsid_C.
INTERPO; IPRO08919; Retrow_capsid_N.
INTERPO; IPRO08919; Retrow_capsid_N.
Pfam; PF02228; Zif_CCHC.
Pfam; PF00209; Zf-CCHC; 2.
PRINTS; PR00939; Zf-CCHC; 2.
PRINTS; PR00939; Zf-CCHC; 2.
PROSITE; PS50158; ZF_CCHC; 1.
COST PROOFIN; POLYPROTEIN; Zinc-finger; Repeat.
CHAIN 131 344 MAJOR CORE PROTEIN P24.
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100.0%; Pred. No. ...
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CCHC-TYPE 2
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Best Local Similarity 100...
5, Conservative
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355
378
429 AA;
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                                                    SECUENCE FROM N.A.
NCBI_TaxID=11927;
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1 HPRPPRGR 8
             Query Match
                                                                                                                                                                                                                                                                                                       Q8H3U2
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Q8H3U2
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                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                 6, 2004, 15:51:34; Search time 28.9346 Seconds (without alignments) 87.236 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                - protein search, using sw model
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Q7U0DS
Q7U0DS
Q84729
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Q848D0
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Q9C591
Q9FPC5
Q8Y1J6
Q84J66
Q84J66
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sp rodent:*
sp virus:*
sp vertebrate:*
sp unclassified:*
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sp_bacteria:*
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sp_bacteriap:*
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sp_phage:*
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Maximum DB seq length: 200000000
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50
1 HPRPPRGR 8
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Match Length
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Perfect score:
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17 39 78.0 346 11 060535 Q60535 mesocricetu  
39 78.0 397 11 Q9EQJ1  
20 39 78.0 470 16 P95542  
21 39 78.0 470 16 P95542  
22 39 78.0 470 16 Q7UIF9 Q6230 mus musculu  
22 39 78.0 517 11 Q803E0  
23 78.0 517 11 Q803E0  
24 39 78.0 517 11 Q803E0  
25 39 78.0 602 5 Q9TM7  
25 39 78.0 602 5 Q9TM7  
26 38 76.0 264 10 Q7VIM9  
27 38 76.0 264 10 Q7VIM9  
28 38 76.0 299 10 Q80551  
28 76.0 299 10 Q80551  
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29 28 38 76.0 299 10 Q80551  
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23 76.0 299 10 Q80551  
24 Q9TM7  
25 Q9TM7  
26 G32 2 Q9TM7  
27 74.0 17 Q9TD88  
29 Q9TM7  
20 Q9T
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ALLGNMEN

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D GRANGE

O 1-MAR-2003 (TERMELTE! 23, Created)

DT 01-MAR-2003 (TERMELTE! 23, Last sequence update)

DE PO418E08.7 protein.

DE PO418E08.7 protein.

SO Orza sativa (japonica cultivar-group).

CC Subrarycola, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

CC Shrhartoidee; Oryza.

CC Shrhartoidee; Oryza.

CC STRAIN=CY Nipponbare;

RN 11

RN 5SQUENCE FROW N.A.

CONTAS asadi T., Mateumoto T., Yamamoto K.;

RN 11

RN 5SQUENCE FROW N.A.

CONTAS asadi T., Mateumoto T., Yamamoto K.;

RN 11

RN 5SQUENCE A07 A4; 43973 MW; D39557777F8252C8 CRC64;

CONSETVANCE 407 A4; 43973 MW; D39557777F8252C8 CRC64;

CONSETVANCE A07 A4; 43977 MACCHOS 11; Indels 0; Gaps

ON 118 HPRPPRGR 8

DD 118 HPRPPRGR 125

RESULT 2

CONSETVANCE A07 CREMELIANINARY; PRT; 561 AA.

AC O05316

DT 01-UUL-1997 (TERMELTE! 04, Created)

DT 01-UUL-1997 (TERMELTE! 04, Created)

DT 01-UUL-1997 (TERMELTE! 04, Created)
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Gaps

us-10-009-709-9.rspt

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MEDLINE 59319331, PubMed=7596291,
MeDLINE 1., Chol K., Yamashita M., Murooka Y.,
Molnar I., Choi K., Yamashita M., Murooka Y.,
"Molecular cloning, expression in Streptomyces lividans, and analysis of a gene cluster from Arthrobacter somplex encoding 3-
ketosteroid-.DELTA.1-dehydrogenaes, 3-ketosteroid-.DELTA.5-isomerase and a hypothetical regulatory protein.",
Mol. Microbiol. 15:895-905(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dziadek J., Yamashita M., Murooka Y.; "Cloning, sequencing and characterization of the downstream region of KsdDl operon of Arthrobacter simplex.";
                                                                                                                                                        Garnier T., Eighmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.Y., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 16; Length 561;
Pred. No. 22;
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86.0%; Score 43; DB 2; Length 545;
Best Local Similarity 87.5%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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Hypothetical protein.
SEQUENCE 545 AA; 57318 MW; 55F441EBD5E3A19E CRC64;
                                                                                                                                                                                                                                                                                                                                                   561 AA; 62626 MW; C35176E8172866AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-071-1997 (TrEMBLrel. 04, Created)
01-071-1997 (TrEMBLrel. 04, Last sequence update)
01-071-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Nocardioides simplex (Arthrobacter simplex).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actino
Propionibacterineae, Nocardioidaceae, Pimelobacter
                        Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 AA.
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Q54729;
01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                     STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
                                                                                                                                                                                                                                                                                                                                                                                                   88.0%;
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Best Local Similarity 87.5'
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534 YPRPPRGR 541
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                                            NCBI_TaxID=1765;
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W.,
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                   MEDINE=98295987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeder K., Gas S., Barry C.E. III, Tekaia F.,

Gordon S.V., Eiglmeder K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornaby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Ruter S., Geeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

Complete genome sequence.";
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                                                              Mycobacterium tuberculosis.
Bacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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TIGK, MT1253, ...
TIGK, MT1253, ...
TUB-crulist; Rv12156, ...
TUB-crulist; Rv12156, ...
TUB-crulist; Rv12156, ...
TUB-crulist; Rv12156, ...
TUB-crulist; Rv1256, ...
TUB-crulist; Rv1256, ...
TUB-crulist; Rv1256, ...
TUB-crulist; Frida binding; IEA.
TUB-crulist; Frida Pro aminopeptidase activity; IEA.
TUB-crulist; Frida Pro aminopeptidase activity; IEA.
TUB-crulist; Frida Proteclysis and peptidolysis; IEA.
TUB-crucy IPRO08979; Gal Dind like.
TUB-crucy IPRO08979; Gal Dind like.
TUB-crucy IPRO08979; Gal Dind like.
TUB-crucy IPRO0893; Peptidase S15.
TUB-crucy IPRO0893; Peptidase S15.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 293777; CAB07817.1;
PIR; AE07002; AAK45510.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62610 MW; 6D2C3253F2D3598D CRC64;
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01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical protein.
  01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein (Diester hydrolase, putative). RV1215C OR MTC1364.27C OR MT1253.
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les 7; Conservative
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PROSITE; PS00037; MYB_1;
Hypothetical protein; Hyd
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534 YPRPPRGR 541
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Q700D5;
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   Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Bhrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).

Dukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Expernatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enthartoideae; Oryzeae; Oryza.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Sasaki T., Matsumoto K.;
Matsumoto T., Yamamoto K.;
"Oryza sariva nipponbare(GA3) genomic DNA, chromosome 7, PAC clone:P0453G03.";
                                                                                                            SEQUENCE FROM N.A.
STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Katayose Y.;
In Matsumoto T., Ratayose Y.;
Cyza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC clone:P0577B11."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%; Score 41; DB 10; Length 633; 75.0%; Pred. No. 78; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                           84.0%; Score 42; DB 10; Length 535; 100.0%; Pred. No. 46; 0; Mismatches 0; Indels
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                                                                                                                                                                                           Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AP005504; BAC57819.1; ...
InterPro, IPR002885; PPR. PFR. PFAMS, PF01535; PPR; PR. 9.
TIGRFAMS, ITGR00756; PPR; 9.
SEQUENCE 535 AA; 58557 MW; C2712C4178582982 CRC64;
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Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
Matches 6; Conserv
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Q48926
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Q7X188
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Eukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
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PubMed=11967531;

Abi-Rached L., Shilas A., Shilas T., Pontarotti P., Inoko H.;

"Evidence of en bloc duplication in vertebrate genomes.";

Nat. Genet. 0:0-0(2002).

Nat. Genet. 0:0-0(2002).

GO, GO:0016491; Foxidoreductase activity; IEA.

GO, GO:0016491; P:metabolism; IEA.

InterPro; IPR008222; Di-copper_centre.
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
00RF11692 (Fragment).
Synechococcus (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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84.0%; Score 42; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                STRAIN=PCC 7942;
Trainoremas N.F., Golden S.S.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U44761; AAA86647.11;
InterPro; IPR001064; Crystallin.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
SEQÜENCE 332 AA; 38574 MW; CA17B5F4B0F2ED09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 494 AA; 56646 MW; 6823A97CDCFA105E CRC64;
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Last annotation update)
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01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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PRINTS, PR00092, TYROSINASE.
PROSITE, PS00497, TYROSINASE_1; 1.
PROSITE; PS00499, TYROSINASE_2; 1.
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Best Local Similarity
7, Conserva
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01-OCT-2003 (TrEMBLr
P0577B11.16 protein.
                                                                                                                                                                                                                                                                                                                                                                                       282 PRPPRGR 288
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                                                                                                                   SEQUENCE FROM N.A.
                                                                                NCBI_TaxID=1140;
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01-JUN-2003
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Q8T777;
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Q84SD0
ID Q84SI
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Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
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Pyrococcus.
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                                                                                                                                                                 MEDLINE=96200863; PubMed=8621098;
Fernandes N.D., Kolattukudy P.E.;
Cloning, sequencing and characterization of a fatty acid synthase-
encoding gene from Mycobacterium tuberculosis var. bovis BCG.";
Gene 170:95-99(1996).
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R GO; GO: 0004312; F:fatty-acid synthase activity; IEA.

GO; GO: 0016491; F:oxidoreducae activity; IEA.

R GO; GO: 0016491; F:transferase activity; IEA.

R GO; GO: 001640; F:transferase activity; IEA.

R GO; GO: 001653; F:fatty acid biosynthesis; IEA.

GO; GO: 0006633; F:fatty acid biosynthesis; IEA.

R InterPro; IPR001327; Actrans.

R InterPro; IPR001327; Actrans.

R InterPro; IPR001395; Fatty acid synth.

R InterPro; IPR001395; Fatty acid synth.

R Ffam; PF00169; Actoacyl synth.

R Ffam; PF00169; Actoacyl synt.; 1.

R Ffam; PF01875; MacC dehydratas; 1.

R Pfam; PF01875; MacC dehydratas; 1.

R PRINTS; PR01483; PASYNTHASE; 1.

R PROSITE; PS01669; B. KETOACYL SYNTHASE; 1.

R PROSITE; PS01666; B. KETOACYL SYNTHASE; 1.
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85.7%; Pred. No. 27;
iive 0; Mismatches 1; Indels
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PIR, F71241, F71241.
Hypothetical protein; Complete proteome.
SEQUENCE 129 AA; 14331 MW; BB551E49F0F8F2F1 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
Hypochetical (TrEMBLrel. 24, Last annotation update)
PH0192.
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MEDLINE=98344137; PubMed=9679194;
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87.5%;
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Best Local Similarity 55...
6; Conservative
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Best Local Similarity 87.5
7; Conservative
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                                                                                                                                    STRAIN=BCG-Pasteur;
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                                                                                SEQUENCE
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STRAIN-GY. Columbia;
Town C.D., Haas B.J., Maiti R., Hannick L.I., Chan A.P., Ronning C.M.,
Town C.D., Haas B.J., Maiti R., Hannick L.I., Utterback T.R., VanAken S.E.,
Smith Jr R.K., Arbogast T., Tallon L.J., Utterback T.R., VanAken S.E.,
Feldblyum T.V., Yu C., Wortman J.R., White O., Fraser C.M.;
"Arabidopsis thallana chromosome 5 BAC F13M11 genomic sequence.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ALS89883; CAC34489.1; --
EMBL; AC140977; AA073898.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last amocation update)
101-JUN-2003 (TrEMBLRel. 24, Last amocation update)
Hypothetical protein (AP2 domain transcription factor, putative)
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Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes
Rudd S., Lemcke K., Mayer K.F.X.,
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95302501; PubMed=7783207;
Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
"The DNA sequence of equine herpesvirus 2.";
"Mol. Biol. 249:520-528(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.0%; Score 39; DB 12; Length 200; 85.7%; Pred. No. 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     Equine herpesvirus type 2 (atrain 86/87) (EHV-2). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae.
                                                                                                                                                                                                                                                                                                                 .-NOV-1996 (TrEMBLrel. 01, Last sequence update)
.-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                      200 AA.
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                                                                                                                                                                                                                                                                                   Created)
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Best Local Similarity 85.
                                                                                                                                                                                                                      PRELIMINARY;
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                                                     83 HPHPPRG 89
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1 HPRPPRG 7
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01-NOV-1996
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Q66619
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Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Frenard C., Cunnac S., Demange N., Sagnier P., Laview M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Welseenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                           78.0%; Score 39; DB 16; Length 246; 75.0%; Pred. No. 70; 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                              246 AA; 24863 MW; 4127DF6A38274F74 CRC64;
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           SEQUENCE FROM N.A.
STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                  EMBL; AL646060; CAD14224.1; -.
InterPro; IPR005184; DUF306.
Pfam; PF03724; NETA; 1.
Complete proteome:
SEQUENCE 246 AA; 24863 NW;
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Matches 6; Conservative
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          FROM N.A.
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Q84J66;
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Q84J66
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        GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0003705; F:structural constituent of ribosome; IEA.
GO; GO:0003706; F:transcription factor activity; IEA.
GO; GO:0006312; P:regulation of transcription, DNA-dependent; IEA.
INTERPRO IPRO01471; FERF.
PFAM: PF00847; AZ2-domain; 1.
PRINTS; PRO0367; ETHRSPELEMY.
ProDom; PD001423; TE FRF; 1.
SWART; SM00380; AP2; 1.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
                                                                                                                                                                                                                                                                 Score 39, DB 10; Length 216;
Pred, No. 62;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                        11 protein.
216 AA; 24400 MW; E8C317B74759056E CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Probable transmembrane protein.
RSC0694 OR RS01599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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(TrEMBLrel. 16, I
(TrEMBLrel. 22, I
                                                                                                                                                                                                                                                                    78.0%;
85.7%;
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Best Local Similarity 100.
Matches 6, Conservative
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P0679C08.18 protein.
P0679C08.18.
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                                                                                                                                                                                                                                                                                                                                 1 HPRPPRG 7
O80337; 2GCC
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                                                                                                                                                                                                                     Hypothetical
SEQUENCE 21
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01-MAR-2001
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RESULT 13

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Hypothetical protein.
OSJNBA0015N08.4 OR OSJNBB0096M04.10.
OSJNBA0015N08.4 OR OSJNBB0096M04.10.
SURVAR astiva (japonica cultivar-group).
Bukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Nipponbare;

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.,
"Oryza sativa chromosome 3 BAC OSJNBAOLENOR genomic sequence.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. Nipponbare; Buell C.K., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Padrosh D.W., Tallon L.S., Neadwuller S.B., Deterback T.T., Peldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Oryza sativa chromosme 3 BAC OSJNBD0096M04 genomic sequence."; submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AC096688; AA020060.1; -. EMBL, AC092559; AA037953.1; -. InterPro; IRRO01660; SAM.
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Hypothetical protein.
SEQUENCE 256 AA; 26728 WW; EC64E19D850D6203 CRC64;
                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
256 AA
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0; Gaps

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Tue Apr 6 17:16:19 2004

Best Local Similarity 100.0%; Pred. No. 72; Matches 6; Conservative 0; Mismatches

1 HPRPPR 6 |||||||| 86 HPRPPR 91

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Search completed: April 6, 2004, 16:14:42 Job time : 30.0115 secs

sw model using OM protein - protein search,

April 6, 2004, 15:29:39 ; Search time 44.785 Seconds (without alignments) 50.472 Million cell updates/sec Run on:

Title: Perfect score:

US-10-009-709-9 50 1 HPRPPRGR 8 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* 1: genesecn1980s.* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Aab48778 Human sal		·	Abb38848 Peptide #	m	Aam72058 Human bon	4 Human	Abg53742 Human liv	Abg41873 Human pep	Human	Abr56769 Human sec	Ada83798 Human PRH	Adc98216 Human sal	Aag58448 Zea mays	0	œ	œ	_	9	ч	œ	ч	85	81
SUMMARIES	~~ ~~	200	AAB48779	AAB48778 / /	17	AAB48783/ /	ABB38848	AAM32323	AAM72058	AAM59494	ABG53742	ABG41873	ABR57423	ABR56769	ADA83798	ADC98216	AAG58448	AAB48780	ABM65798	ABG18278	AAU65747	ABM62266	ABG26281	ABG03818	ADE07941	ABG70853	ABP76681
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Abu79133 Mycobacte Abp70785 Human ext Aay68970 Germline Abg14712 Novel hum Aau54627 Propionib Abm51146 Propionib Aau64324 Propionib	Propic Human Propic Propic Human		Abm45409 Propionib Aam4187 Human pol Abu34745 Protein e
ABU79133 ABP70785 AAY65870 ABG14712 AAU54627 AAU54146	ABM60843 AAO01213 AAU57069 ABM53588 ABB15815	ABG14998 AAE30036 ABG14713 AAC05792 AAU48890	ABM45409 AAM41387 ABU34745
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ALIGNMENTS

AAB48779 standard; peptide; 8 AA RESULT 1 AAB48779

AAB48779;

(first entry) 09-MAR-2001 Human saliva PRP-1 fragment (residues 101-108), SEQ ID NO:9

Human, PRP-1; proline-rich protein; saliva; dental caries; chromosome 12p13.2; arginine catabolism; ammonia production; pH increase; oral bacterium; caries prevention.

Homo sapiens.

WO200069890-A1.

23-NOV-2000.

11-MAY-2000; 2000WO-SE000930.

L7-MAY-1999; 99SE-00001773.

(STRO/) STROEMBERG N. (JOHA/) JOHANSSON I.

Stroemberg N, Johansson I;

WPI; 2001-031923/04.

New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.

Claim 4; Page 24; 36pp; English

The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12pl3.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for mutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-

AESULT 2

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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being argininerich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-derived oligopeptides of the invention
                                                                                                                                                                                                              Human, FRP-1; proline-rich protein, saliva, dental caries, chromosome 12p13.2; arginine catabolism; ammonia production; pH increase, oral bacterium; caries prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oll gopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.
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                                                                                                                                                                          Human saliva PRP-1 fragment (residues 99-108), SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB48783 standard; peptide; 17 AA.
                                                   AAB48777 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 24; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-2000; 2000WO-SE000930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johansson I;
                                                                                                                                         (first entry)
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nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STRO/) STROEMBERG N. (JOHA/) JOHANSSON I.
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                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                         09-MAR-2001
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             RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia the catabolism of arginine the ammonia of the converted to ammonia by these bacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, PRP-1; proline-rich protein, saliva, dental caries,
chromosome 12p13.2; arginine catabolism, ammonia production, pH increase,
oral bacterium, caries prevention.
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                                                                                Length 8;
                                                                                                                       0; Indels
                                                                              100.0%; Score 50; DB 4; I
100.0%; Pred. No. 1.4e+06;
                                                                                                                           0; Mismatches
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derived oligopeptides of the invention
                                                                                                                                                                                                                                                                                                                   AAB48778 standard; peptide; 9 AA.
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Best Local Similarity luv...
Best Local Similarity
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                                                                                                                           8; Conservative
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                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                      1 HPRPPRGR
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                                          Sequence 8 AA;
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Gaps

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Human; PRP-1; proline-rich protein; saliva; dental caries;

HPRPPRGR 9

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ABB38848 standard; peptide; 132 AA.
                                                                                                                                      Claim 2; Page 24; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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                                                  11-MAY-2000; 2000WO-SE000930
                                                               99SE-00001773
                                                                                            Stroemberg N, Johansson I;
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                              (STRO/) STROEMBERG N.
                                                                                 (JOHA/) JOHANSSON I.
                                                                                                                                                                                                                                                                      œ
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                                                                                                                                                                                                                                    Sequence 17 AA;
                            WO200069890-A1
                                                               17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                 Homo sapiens
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                                        23-NOV-2000
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ABB38848
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
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                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 31483; 639pp + Sequence Listing; English.
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30-UUN-2000; 2000US-02068408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                            Chen W,
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
7-SEP-2000; 2000US-0235959.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                            Hanzel DK,
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26-MAY-2000;
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Matches
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      arginine catabolism; ammonia production; pH increase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                              oral bacterium; caries prevention
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.

DR;

Chen W, Rank

DK,

Penn SG,

WPI; 2001-488897/53

(MOLE-) MOLECULAR DYNAMICS INC

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Gaps ; 0

1 HPRPPRGR 8

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AAM59494 standard; protein; 132 AA.
                                   83 HPRPPRGR 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing
                                 The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                                                                                                       100.0%; Score 50; DB 4; Length 132; 100.0%; Pred. No. 3.8; o; Mismatches 0; Indels
                                                                                                                                                                                                                                            0; Indels
Claim 27; SEQ ID NO 32592; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAM72058 standard; protein; 132 AA.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                         83 HPRPPRGR 90
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Best Local Similarity
                                                                                                                                                                      Sequence 132 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzhaimer's disease, multiple solerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                           Human, brain expressed exon, gene expression analysis, probe; microarray, Alzheimer's disease; multiple sclerosis, schizophrenia, epilepsy; cancer.
                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 31599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG53742 standard, peptide; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0207456P.
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(First entry)
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les 8; Conserv
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                                                                                                                                                                                                                                                            WO200157275-A2
                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000;
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05-NOV-2001
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The invention relates to a single exon nucleic acid probe (SBNP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. Associated secon encoded peptides of the invention. Note: The sequence lifermation for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human peptide encoded by genome-derived single exon probe SEQ ID 31538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
                           Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 50; DB 4; Length 132; larity 100.0%; Pred. No. 3.8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glaim 27; SEQ ID NO 32390; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             but was obtained in electronic format dir
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG, Hanzel DK, Chen W, Rank DR;
Human liver peptide, SEQ ID No 32390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG41873 standard; peptide; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                           2000US-0207456P.
2000US-00608408.
2000US-00632366.
                                                                                                                                                                                                                                                                                               21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                       WO200157273-A2.
                                                                                                                                                                                                                                            26-MAY-2000;
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                                                                                       Homo sapiens.
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Matches
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Gaps

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived cucleic acid probes for measuring gene expression in a sample derived from thuman lung comprising single exon nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 1218 complements or the 12387 open reading frames derived from the 1218 probes. Also included are a microarray comprising the novel set of probes conferences of the professed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a sample collection of detectably labeled nucleic acids derived from human lung measuring the label detectably bound to each probe of the array, identifying exons in a eukaryotic cange from genomic sequences of the eukaryote; and (b) measuring the label detectably bound to each probe of the entangent of detectably measuring the array of the expression of each of the exon probe in the above mentioned microarray assigning exons to a single exon probe in the above mentioned microarray assigning exons to a single exon microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene, of comprising (a) identifying exons from genomic sequence by the method issues and/or call types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of exons should be assigned to a single gene, a peptide comprising of the exons in a gene, particularly using human companies. Or probes/open reading frames (ORF). The probes are used for gent expression of each of the exons in a gene particularly using human under the second or probes/open reading frames (ORF). The probes are used for gent expression of each of the exons should be assigned to a single gene, a peptide comprising of disease (ILD), familial diopathic pulmonary disease (CDP), interactivillar years of diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spatially-addressable set of single exon nucleic acid probes, used to
pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID NO 31538; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                03.AUG-2000; 2000US-00623366.
21.SEP-2000; 2000US-0234687P.
27.SEP-2000; 2000US-0236359P.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-114183/15.
                                                                                                                                                     WO200186003-A2
                                                                                                                                                                                             15-NOV-2001.
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Sequence 132 AA;

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ACF03547 to ACF03570 encode the human NOVX proteins (1) given in ABR57412 to ABR57435. (1) have cytostatic, cardiant, antinflammatory, nootropic, immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic, antiarterioscleroric, anorectic, antiasthmatic, nephrotropic, virucide, antiarthritic, hepatotropic, antiasthmatic, nephrotropic, virucide, antiparasitic, anticonvulsant, hypotensive, vasotropic, antiparkinsonian, vulnerary, angiogenic and antiangiogenic activities, and can be used in gene therapy and vaccines. The NOVX polypeptides and their antibodies can be used to determine the presence or absence of (1) in a sample. The NOVX
                                                                                                                                                                                                                                                                                                                                                                                    Human; NOVX, cytostatic; cardiant; antiinflammatory; immunosuppressive; antialergic; haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; antialergic; hepatotropic; antiarthritic; hepatotropic; neuroprotective; notropic; antibaterial; virucide; antiparasitic; relaxant; anticorropic; antibaterial; virucide; antiparasitic; relaxant; anticorropic; antiparasitic; anticorropic; anticorropic; antiparasitic; relaxant; anticorropic; antiparasitic; anticorropic; anticorropic; anticorropic; antiparasitic; cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; AlDS; obesity; asthma; acquired immunodificiency syndrome; nephropathy; cirrhosis; arthritis; muscular dystrophy; epilepsy; wasting disorder; chromosome 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NOVX polypeptide useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grosse WM, Macdougall JR, Smithson G, Millet I, Stone DJ;
Gunther E, Ellerman K, Alsobrook JP, Lepley DM, Burgess CE;
Spytek KA, Bdinger SR, Gangolli EA, Gorman L, Taupier RJ, Li L;
Guo X, Fernandes ER, Vernet CAM, Tchernev VT, Casman SJ, Shenoy S;
Mishra V, Furtak K, Baumgartner JC, Colman SD;
                                          0; Gaps
  5; Length 132;
                                        0; Indels
100.0%; Score 50; DB 5
100.0%; Pred. No. 3.8;
ative 0; Mismatches
                                                                                                                                                                                                                          ABR57423 standard; protein; 149 AA.
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                                                                                                                                                                                                                                                                                                                                                   Human NOV7 protein SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-2000; 2000US-0245291P.
02-NOV-2000; 2000US-0245317P.
07-NOV-2000; 2000US-024652P.
26-NOV-2001; 2000US-0264389P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JAN-2001; 2001US-0264423P.
29-JAN-2001; 2001US-0264799P.
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                                                                                                                                                                                                                                                                                                         .5-SEP-2003 (first entry)
  Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-140359/13.
                                                                                                                        83 HPRPPRGR 90
                                                                                  1 HPRPPRGR 8
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ABR57423
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polypeptides, polynucleotides encoding them, and antibodies against them, are useful in manufacturing a medicament for treating or preventing a syndrome associated with a NOVX-associated disorder such as hypertension, cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation, autoimmune disorders, allergies, blood disorders, obesity, acquired immunodeficiency syndrome (AIDS), immunoglobulin (Ig)A nephropathy, cirthosis, arthitis, Alzheimer's disease, Parkinson's disease, goite, infections (e.g. bacterial, viral, parasitic), stroke, muscular diseases. ACPO3571 to ACF03644 represent PCR primers and probes for NOVX sequence, which are used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; SECP; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; gene therapy; cancer; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allergy; AIDS; inflammatory disorder; developmental disorder; hypothyroidism; Cushing's syndrome; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang TY, Warren BA, Gietzen KJ, Lal PG, Yue H, Honchell CD, Lehr-Mason PM, Burford N, Xu Y, Baughn MR, Duggan BM, Tran UK, Lee EA, Forsythe IJ, Richardson IW, Lee S, Thangavelu K, Yue H, Benrling BM, Walia NK, Azimzai Y, Sanjanwala B, Hafalia AJA; Borowsky ML, Nguyen DB, Ison CH, Astromoff A, Ding L, Lee SY, Becha SD, Ramkumar J, Gandhi AR, Jin P, Pu GK, Swarnakar A;
                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                     100.0%; Score 50; DB 6; Length 149; 100.0%; Pred. No. 4.2; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein SECP-44 SEQ ID NO:44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR56769 standard; protein; 154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-AUG-2001, 2001US-0313249P.
24-AUG-2001, 2001US-0314752P.
07-SEP-2001, 2001US-0317818P.
07-SEP-2001, 2001US-0317818P.
21-SEP-2001, 2001US-031886P.
24-SEP-2001, 2001US-034586P.
28-NOV-2001, 2001US-034380P.
13-FEB-2002, 2001US-0343229P.
13-FEB-2002, 2002US-0365243P.
19-WAR-2002, 2002US-0366041P.
30-APR-2002; 2002US-0366041P.
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                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100...
Best as 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUL-2003 (first entry)
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N-PSDB; ACC79069.
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                                                                                                                                                                                                                                      Sequence 149 AA;
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ACC79026 to ABR56805, designated SECP-1 to SECP-80. SECP sequences can ABR56726 to ABR56805, designated SECP-1 to SECP-80. SECP sequences can have overceative, antiatrerisosclerotic, anticonvulsant, antialial ammatory, notropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic and thyromimetic activities, and can be used in dagnosing, treating and preventing and polyvucleotides can be used in dagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of SECP, such as cell proliferative (e.g. expression or overexpression of SECP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and calculons. They are also useful in assessing the effections. They are also useful in assessing the effections or in a fragments are useful in screening compounds for effectiveness as agoing or antagonist of the polypeptides, or in altering the expression of the target polyuncleotide and compounds that specifically bind to or modulate the activity of the polypeptide
                   New human secreted proteins (SECP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant SECP expression e.g. cancer, AIDS, atherosclerosis, Huntington's disease, stroke, infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA83798 standard; protein; 166 AA.
                                                                                                                                                                                                             Claim 1; Page 222; 286pp; English.
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22-OCT-2001; 2001US-0330457P.
19-FEB-2002; 2002US-0357144P.
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(first entry)

Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all BSTs expressed in normal

Krukovskaya LL;

Lobashev AV,

Baranova AV, Yankovsky NK, Kozlov AP,

WPI; 2003-175241/17.

N-PSDB; ADA83797

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Gaps ö

100.0%; Score 50; DB 6; Length 154; 100.0%; Pred. No. 4.3; tive 0; Mismatches 0; Indels

Conservative

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The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTS) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue of in order to identify ESTs that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably carbidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hypersometic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful as an end of the invention is useful as an end of immenogen for vaccinating a main animal. The present sequence represents a consecut of the invention is also useful as an animal. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Atopic dermatitis-inducing proteins, applicable in diagnosis of including risk of onset, and in developing sensitization remedies for the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; salivary acidic proline-rich phosphoprotein; PRP; autoantigen; atopic dermatitis-inducing protein; salivary gland; IgE autoantibody; imminoglobulin B; mast cell activation; basophil activation; diagnosis risk assessment; sensitisation remedy; dermatological; antiallergic; antiinflammatory.
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                                 Claim 29; Page 191-192; 516pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC98216 standard; protein; 166 AA
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The invention relates to the human atopic dermatitis-inducing proteins, salivary acidic proline-rich phosphoprotein (PRP; ADC98216) and prolactin cinducible protein (PIP) and their post-translationally modified forms. These proteins are secreted by salivary or sweat glands and bind to IgE autoantibodies, thereby activating mast cells and PRP or PIP; antibodies which bind to PRP or PIP, methods for diagnosing atopic dermatitis or for determining whether an individual is at risk of developing atopic dermatitis by determining the presence of PRP- or PIP-specific antibodies or immune complexes, or by quantifying histamine release; and sensitisation remedies for atopic dermatitis containing PRP and/or PIP or their peptides as the active ingredient. PRP, PIP and their an individual is at risk of developing atopic dermatitis. They whether an individual is at risk of developing atopic dermatitis. They are also useful in diagnosing atopic dermatitis containing proper are also useful in diagnosing sensitisation remedies for the treatment of atopic dermatitis. They active increases the specifically atopic dermatitis in the present sequence represents the specifically atopic dermatitis in the present sequence represents the specifically claimed human salivary acidic proline-rich phosphoprotein (PRP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                              100.0%; Score 50; DB 7; Length 166; 100.0%; Pred. No. 4.6; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG58448 standard; protein; 51 AA.
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99US-0125788P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                               117 HPRPPRGR 124
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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01-APR-1999;
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PR 14-May 1999 9905-0144216P.

PR 14-May 1999 9905-0144219P.

PR 14-May 1999 9905-0144768P.

PR 22-May 1999 9905-0144768P.

PR 24-May 1999 9905-0144768P.

PR 24-May 1999 9905-0144768P.

PR 24-May 1999 9905-015622P.

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PR 04-UM-1999 9905-015622P.

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PR 16-UM-1999 9905-0137524P.

PR 16-UM-1999 9905-0137524P.

PR 16-UM-1999 9905-0139453P.

PR 22-UM-1999 9905-0139453P.

PR 13-UM-1999 9905-0139453P.

PR 13-UM-1999 9905-0139453P.

PR 13-UM-1999 9905-0140632P.

PR 13-UM-1999 9905-0142058P.

PR 13-UM-1999 9905-014332P.

PR 13-UM-1999 9905-014333P.

PR 13-UM-1999 9905-0144333P.

PR 13-UM-1999 9905-014433P.

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9904S-0145218P

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Gaps
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0
                                                                                                                                 Score 44, DB 3, Length 51;
Pred. No. 13;
0; Mismatches 1; Indels
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99US-0160981P.
99US-01660989P.
99US-0161405P.
99US-0161405P.
99US-0161360P.
99US-0161361P.
99US-0161361P.
99US-0161930P.
99US-0161932P.
                                                                                                                                 Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                   |||||| |
23 HPRPPRSR 30
                                                                                                                                                                        1 HPRPPRGR 8
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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28-0CT-1999;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 6, 2004, 16:14:50 ; Search time 31.4019 Seconds (without alignments) 66.909 Million cell updates/sec Run on:

US-10-009-709-9 50 1 HPRPPRGR 8 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1071772 seqs, 262633353 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA: *

1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCCMB.pep: *

2: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *

3: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *

4: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *

6: /cgm2_6/ptodata/1/pubpaa/US06_PUBCCMB.pep: *

6: /cgm2_6/ptodata/1/pubpaa/US08_PUBCCMB.pep: *

7: /cgm2_6/ptodata/1/pubpaa/US08_PUBCCMB.pep: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 43644, A	Sequence 80, Appl	Sequence 69167, A	Sequence 43478, A	Sequence 223703,	Sequence 7, Appli	Sequence 114, App	Sequence 114, App	Sequence 178111,	Sequence 174830,	Sequence 239718,	Sequence 66403, A	Sequence 62669, A	Sequence 5, Appli	Sequence 29711, A
SUMMAKIES ID	US-09-864-761-43644	US-10-157-031-80	US-10-425-114-69167	US-10-425-114-43478	US-10-424-599-223703	US-10-084-846A-7	US-09-870-759-114	US-09-751-708A-114	US-10-424-599-178111	US-10-424-599-174830	US-10-424-599-239718	US-10-425-114-66403	US-10-282-122A-62669	US-10-406-209-5	US-10-029-386-29711
DB		14	12	12	12	15	σ	70	12	12	12	12	12	14	14
% Query Match Length DB	132	166	238	277	72	19652	2796	2796	71	164	198	278	470	618	99
% Query Match	100.0	100.0	90.0	0.06	84.0	84.0	82.0	82.0	78.0	78.0	78.0	78.0	78.0	78.0	76.0
Score	50	50	45	45	42	42	43	41	39	9	თ ო	ტ ტ	39	ტ ტ	38
Result No.	1	61	٣	4	'n	φ	7	œ	σι	10	11	12	13	14	15

Sequence 285441, Sequence 6771, Ap		106,	9	38759,	Seguence 151579,	Sequence 1824, Ap	Sequence 191513,	Sequence 52873, A	Sequence 245792,	Sequence 69576, A	Sequence 14830, A	GENERAL INFORMA	Seguence 2741, Ap	Sequence 1429, Ap	Sequence 38, Appl	Sequence 2734, Ap	Sequence 59553, A	Sequence 279857,	Seguence 60421, A		6, App	9 66,	54425,	5204	5196	70,	Sequence 69, Appl	Sequence 18, Appl
-599-285	US-10-425-114-7	4 US-10-008-524A-10	5 US-10-350-719	US-09-864-761-3875	2 US-10-424-599-15	US-09-925-300-1	2 US-10-424-599-1	2 US-10-425-11	2 US-10-424-599-245792	US-10-425-11	US-10-156-76	. US-10-457-37	വ	6 US-10-389-566-14		5 US-10-108-260A-2734	2 US-10-425-114-5955	2 US-10-424-599-2798	2 US-10-425-114-60	5 US-10-369-493-502	US-09-827-822-	4 US-10-157-031-6	US-10-425-114-54	US-10-425-114-5204	US-10-425-114-5	US-09-981-15	1 US-09-981-151A-69	
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ALIGNMENTS

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Sequence 43644, Application US/09864761

Patent No. US20020048763M1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                        THILE CHINGALIAN GENE EXPRESSION ANALISMS
CURRENT APPLICATION NUMBER: US/09/664,761
CURRENT APPLICATION NUMBER: US/09/664,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-06-3
PRIOR PELING DATE: 2000-09-3
PRIOR PLING DATE: 2000-09-3
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 06/236,359
PRIOR PLING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
US-09-864-761-43644
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RESULT 4

US-10-425-114-43478

US-10-425-114-43478

US-10-425-114-43478

Sequence 43479, Application US/10425114

Publication No. US20640034888A1

Septiment Into US/20640034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Kovalit, David K.

APPLICANT: Soreen, Steven E

APPLICANT: Tabask, Jack E

APPLICANT: Cao, Yongwei

ITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TILE OF INVENTION NUMBER: USA10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
                                                                                  APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Exou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 10201313)B
TITLE FERENCE: 1201313)B
TITLE FERENCE: 12003-04-28
UNRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 63167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.0%; Score 45; DB 12; Length 238; 100.0%; Pred. No. 57; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Clone ID: UC-ZMFLMO17307C10_FLI.pep
US-10-425-114-69167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE;
; OTHER INFORMATION: Clone ID: 700423863_FLI.pep
US-10-425-114-43478
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                    Publication No. US2004003488A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 7; Conservative
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-424-599-223703
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LENGTH: 277
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FUBLICARIE BERROAVA A. V.

APPLICANT: Baranova, A. V.

APPLICANT: Kozlov, A. P.

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OTHER INFORMATION: EXPRESSED IN PLACENRA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PRIAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PRIAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN BADLA LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: SYRISSPROT HIT: BF088785.1, BVALUE 1.00e-01
US-09-864-761-43644
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Best Local Similarity 100.0%; Pred. No. 8.4; Length 166;
Matches 8; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 50; DB 9; Length 132;
Best Local Similarity 100.0%; Pred; No. 6.9;
Matches 8; Conservaive 0; Mismatches 0; Indels
Matches 9; Conservaive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-09-31
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49177
SEQ ID NO 43544
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; Sequence 69167, Application US/10425114
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CRGANISM: Homo sapiens
US-10-157-031-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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Matches
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Score 39; DB 12;
Pred. No. 1.4e+02;
1; Mismatches 0;
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Pred. No. 1.7e+03;
0; Mismatches 1;
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87.5%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT;
CRGANISM: Mycobacterium bovis
US-09-751-708A-114
                                                                                                                                                                                                                                                                                                    Query Match 82.0%;
Best Local Similarity 87.5%;
Matches 7; Conservative (
                                                                                                                              NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 114
LENGTH: 2796
                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Mycobacterium bovis
US-09-870-759-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.0
Best Local Similarity 87.5
Matches 7; Conservative
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILE REPERRICE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 223703

LENGTH: 72

TYPE
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Patent No. US20020177551A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REPERENCE: 870759
CURRENT APPLICATION NUMBER: US/99/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 2.
OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

84.0%; Score 42; DB 12; Length 72;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_44033C.1.pep
US-10-424-599-223703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10084846A

| Sequence 7, Application US/10084846A
| Publication No. US20040006026A1
| GENERAL INFORMATION:
| APPLICANT: WEITNAUER, GABES
| APPLICANT: MILLENWEG, AGNES
| APPLICANT: MILLENWEG, AGNES
| APPLICANT: BECHTHOLD, ANDREAS
| TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
| TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
| TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
| TITLE REFERENCE: 1974-005
| CURRENT FILING DATE: 2003-02-25
| PRIOR APPLICATION NUMBER: DE 101 09 166.4
| PRIOR PILING DATE: 2001-08-24
| PRIOR PILING DATE: 2001-02-25
| NUMBER OF SEC ID NOS: 120
| SOFTWARE: PATENTIN OFT: 3.2
| SEQ ID NO 7.
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Best Local Similarity 100.
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US-09-870-759-114
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Sequence 178111, Application US/10424599
Publication No. US2004001072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Can Varior David K
APPLI
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Sequence 114, Application US/09751708A

Sequence 114, Application US/09751708A

PUDIcation No. US20030157113A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: 751708

CURRENT APPLICATION NUMBER: US/09/751,708A

CURRENT FILING DATE: 2002-10-15

FRIOR APPLICATION NUMBER: US 60/173,371

PRIOR PILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 166

SOFTWARE: Patentin version 3.1

SEQ ID NO 114

LENGTH: 2796
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Pred. No. 1.7e+03;
0; Mismatches 1; Indels (
Length 2796;
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; CTHER INFORMATION: Clone ID: PAT_MRT3847_131850C.1.pep
US-10-424-599-178111
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PRPPRGR 8

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Sequence 174830, Application US/10424599
PUblication No. U220040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Valic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 174830
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APPLICANT: La Rosa Thomas J
APPLICANT: Xovalic David K
APPLICANT: Xovalic David K
APPLICANT: Xovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5323) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 239718
LENGTH: 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.0%; Score 39; DB 12; Length 164; 75.0%; Pred. No. 2.9e+02; tive 1; Mismatches 1; Indels
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US-10-424-599-174830
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COTHER INFORMATION: Clone ID: PAT_MRT3847_58490C.1.pep US-10-424-599-239718
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US-10-424-599-239718
Sequence 229918, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Matches 6; Conservative
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ORGANISM: Glycine max
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            61 PRPPRGK 67
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US-10-424-599-174830
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| Sequence 66403, Application US/10425114
| Sequence 66403, Application US/10425114
| Publication No. US20040034888A1
| GENERAL INFORMATION:
| APPLICANT: Liu, Jingdong
| APPLICANT: Liu, Jingdong
| APPLICANT: Screen, Saven E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Tabaska, Ja
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FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
FRIOR PELICATION NUMBER: 05/191,078
FRIOR PILING DATE: 2000-03-21
FRIOR PILING DATE: 2000-03-21
FRIOR PILING DATE: 2000-03-21
FRIOR PILING DATE: 2000-03-23
FRIOR PILING DATE: 2000-03-26
FRIOR PILING DATE: 2000-03-26
FRIOR FILING DATE: 2000-03-06
FRIOR FILING DATE: 2000-03-06
FRIOR FILING DATE: 2000-03-09
FRIOR PILING DATE: 2000-10-23
FRIOR PILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR PILING DATE: 2000-11-27
FRIOR PILING DATE: 2000-11-27
FRIOR PILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-10-20
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78.0%; Score 39; DB 12; Length 278;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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Sequence 62669, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John
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: Carr, Grant
Yamamoto, Robert
Forsyth, R.
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RESULT 12
US-10-425-114-66403
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TYPE: PRT
ORGANISM: Homo sapiens
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Matches 6; Conserv
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Publication No. US2030194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharid R.
APPLICANT: Penn, David R.
APPLICANT: HUARN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: HUARN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REPRESENCE: ABOUNCA.*2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT PILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOSTWARE: Annomax Sequence Listing Engine vers. 1.1
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JAPPLICANT: KYOWA HAKKO KOGYO CO., LTD.

TITLE OF INVENTION: NOVEL ANTIBODIES, DRUGS CONTAINING THESE ANTIBODIES AND TITLE OF INVENTION: NOVEL ANTIBODIES, DRUGS CONTAINING THESE ANTIBODIES TITLE OF INVENTION: SCREENING COMPOUNDS BY USING THESE ANTIBODIES FILE REPERENCE: 1241.18

FILE REPERENCE: 1241.18

CURRENT FILING DATE: 2003-04-04

PRIOR FILING DATE: 2001-08-30

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29

PRIOR PEDILOCATION NUMBER: EARLIER APPLICATION NUMBER: UP 10-291501

PRIOR PEDILOCATION NUMBER: EARLIER FILING DATE: 1998-09-29

PRIOR PEDILOCATION NUMBER: EARLIER FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 28

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PARCHER FILING DATE: 1998-09-29
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILIMG DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 62669
LENGTH: 470
                                                                                                                                                                                                                                                                                      78.0%; Score 39; DB 12; Length 470; ilarity 85.7%; Pred. No. 7.2e+02; Conservative 0; Mismatches 1; Indels
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US-10-406-209-5
Sequence 5, Application US/10406209
Publication No. US20030170758A1
GENERAL INFORMATION:
                                                                                                                                                                                     TYPE: PRT ORGANISM: Mycobacterium bovis
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Best Local Similarity
Thes 6; Conserve
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US-10-029-386-29711
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FEATURE:

ORGANISM: Home sapiens

FEATURE:

ORGANISM: Home sapiens

FEATURE:

OTHER INFORMATION: MAP TO CHRIL: I

OTHER INFORMATION: EXPRESSED IN FLACENTA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEALY, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEALY, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: SWISSPROT HIT: P03291, EVALUE 3.50e+00

US-10-029-386-29711

Query Match

G. CONSELVATIVE 0; Mismatches 1; Indels 0; Gaps

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Search completed: April 6, 2004, 17:06:07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106, App
20099, A
21772, A
32430, A
7, Appli
                                                                               April 6, 2004, 15:56:34; Search time 11.7383 Seconds (without alignments) 35.185 Million cell updates/sec
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Sequence
Sequence
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/cgm2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-17072
US-09-252-991A-17072
US-09-252-991A-16736
US-09-252-991A-16736
US-09-252-991A-24713
US-09-252-991A-24713
US-09-252-991A-31918
US-09-252-991A-31918
US-09-252-991A-31856
US-09-352-991A-3063
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US-09-252-991A-32430
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US-08-469-260A-38
US-08-488-446-38
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                                                                                                                                                                                                                                                       389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                        - protein search, using sw model
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Gapop 10.0, Gapext 0.5
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Maximum DB seq length: 2000000000
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ALIGNMENTS

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RESULT 1
19-92-521-991A-29452
19-90-252-991A-29452
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19-92-291A-29452
19-92-291A-29452
19-92-291A-29552
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Sequence 16736, Application US/09252991A

Sequence 16736, Application US/09252991A

Sequence 16736, Application US/09252991A

Setent No. 6531736

GENERAL INFORMATION:

APPLICANT: MACE J. RUBERTIAL OF SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 33142

LENGTH: 439
                                                         KERULT Sequence 31405

VS-09-252-991A-31405

Sequence 31405 Application US/0925291A

Fatent No. 6551195

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

FRIOR APPLICATION NUMBER: US 60/074,768

FRIOR APPLICATION NUMBER: US 60/074,768

FRIOR APPLICATION NUMBER: US 60/074,190

FRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 152

LENGTH: 152
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| Sequence 24713, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION RUCKEL OF THE OF INVENTION INCLUDED AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS | TITLE OF INVENTION. ARGUINOSA FOR DIAGNOSTICS AND THERAPEUTICS | FILE REPERRING: 107196, 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136 | 136
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87.5%; Pred. No. 18;
tive 0; Mismatches 1; Indels
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82.0%; Score 41; DB 4; Length 439;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 1; Indels
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ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
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Matches 7; Conservative
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WS-09-252-991A-17072

Sequence 17072, Application US/09252991A

Sequence 17072, Application US/09252991A

Sequence 17072, Application US/09252991A

Sequence 17072, Application US/09252991A

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Ruchelc Acid Anno Acid Sequences Relating To Pseudomonas

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 223
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US-09-252-991A-24480

Sequence 24480, Application US/09252991A

Sequence 24480, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-17

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24480

LENGTH: 559
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84.0%; Score 42; DB 4; Length 559;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                  Query Match 84.0%; Score 42; DB 4; Length 207; Best Local Similarity 100.0%; Pred. No. 17; Matches 7; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29505
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Patent No. 6551795

Sequence 30229, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc N. ULCLEIC AID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: ACIDICALION AND THERAPEUTICS
FILLS REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30229

LENGTH: 420
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: MUCLEIC AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 107136 / 136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR SEQ ID NOS: 33142
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                                          78.0%; Score 39; DB 4; Length 302; 85.7%; Pred. No. 68; 1; Indels tive 0; Mismatches 1; Indels
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; Patent No. 6551795
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30229
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ORGANISM: Pseudomonas aeruginosa
               Query Match
Best Local Similarity 85.7%
....hes 6; Conservative
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Best Local Similarity 85./*
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US-09-252-991A-30229
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US-09-552-991A-31918

i Sequence 3191B-1, Application US/09252991A

i Sequence 3191B-1, Application US/09252991A

i Sequence 3191B-1

i Batent No. 651795

i GENERAL INFORMATION:

i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

I TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

I TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 302
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PAPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO S3933

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82.0%; Score 41; DB 4; Length 676;
Best Local Similarity 87.5%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 1; Indels
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23933, Application US/09252991A
Patent No. 6521795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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Best Local Similarity
Matches 6; Conserv
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Sequence 321594, Application US/09252991A
| Sequence 3215784, Application US/09252991A
| Sequence 3215784, Application US/09252991A
| Patent No. 6551795|
| GENERAL INFORMATION:
| APPLICATION:
| APPLICATION:
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US/09/252,991A
| PRIOR PLICATION NUMBER: US 60/074,788
| PRIOR PLICATION NUMBER: US 60/074,788
| PRIOR PLICATION NUMBER: US 60/094,190
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| SEMICAL APPLICATION NOS: 33142
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREQUINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AREQUINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE OF PREPICATION NUMBER: US/09/252,991A
PRIOR PPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US/00/94,190
PRIOR FILING DATE: 1998-07-27
NUMBER: US/00/94,190
NINGER OF SEQ ID NOS: 33142
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| Patent No. 6551795
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICANT: Marc J. Rubenfield et al. APPLICANT: Marc J. REPERION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS | TITLE OF INVENTION: MERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS | FILE REPERENCE: 107196.136 | CURRENT PELLING DATE: 1999-02-18910A | CURRENT FILING DATE: 1999-02-18910A | PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.0%; Score 39; DB 4; Length 594; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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909-252-91A-28230
Sequence 28230, Application US/09252991A
Patent No. 6521795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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US-09-252-991A-32578
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APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

SEQ ID NOS: 33142

SEQ ID NO 30663

LENGTH: 259
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77.0%; Score 38.5; DB 4; Length 471;
Best Local Similarity 72.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 1; Indels
PRIOR FILING DATE: 1998-02-18
PRIOR PELLING NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 471
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US-09-252-991A-30663

/ Sequence 30663, Application US/09252991A

/ Patent No. 6551795

/ GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: April 6, 2004, 16:19:41 Job time : 12.7383 secs
                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31856
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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 6, 2004, 15:52:34; Search time 7.85047 Seconds Run on:

(without alignments) 85.771 Million cell updates/sec

US-10-009-709-10 1 PRPPRGR 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		livary prol				н		ical	W09G1	ical	-	E	ŭ	b	ď	gag polyprotein -		anthranilate synth		hypothetical prote		latrophilin-1, bra	ın - r	, br	CLIAB protein - ra	CLIBB protein - ra	protein F3F9.20 [i	cholecystokinin B	choled	gastrin receptor -
SUMMARIES	1																													
SUMM	1	55	2537	A27307	E70610	855609	AB3238	D72579	A88637	H82546	D40595	A24026	T32737	FOLJGH	FOLJCN	806073	B72654	B87484	8856	102	1713	1841	1714	T18413	1714	1715	9681	9	4	-
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Score	1 1	42	42	42	42	39	33	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	36	36	36	36
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cholecystokinin B	gastrin/cholecysto	gastrin receptor -	ethylene receptor	ethylene receptor	probable phenylala	ksr protein - frui	latent transformin	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	L2 protein - rhesu	trophoblast-endoth	heterogeneous nucl	exoribonuclease [i
A46195	JC2459	832817	T07026	T07794	T36829	T13856	A55494	T30010	S75053	G83636	D84335	P2WLR1	A46419	T02673	AG2736
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452	452	453	519	635	840	1003	1820	1974	264	352	433	466	550	633	784
85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	83.3	83.3	83.3	83.3	83.3	83.3	83.3
36	36	36	36	36	36	36	36	36	35	35	35	35	35	35	35
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	PRH2	4
	precursor	イフ・ス・ロロ ・ しつい
	phosphoprotein	
RESULT 1 PIHISC	salivary proline-rich phosphoprotein precursor PRH2	N. N. to most o nesson. nesting my saidid not line with not

[validated] - human

N'Alternate names: salivary acidic proline-rich protein PRH2
N'Concains: peptide P C (basic proline-rich peptide 1B-8b); proline-rich phosphoprotei
N'Concains: peptide P C (basic proline-rich peptide 1B-8b); proline-rich phosphoprotei
C'Species: Homo sapiens (man)
C'Date: 31-Mar-1981 #sequence revision 12-Apr-1996 #text_change 08-Dec-2000
C'Accession: As23372; A92037; A92254; A9425; A91954; S02564; S02563; J
R'Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O.
J. Biol. Chem. 260, 11123-11130, 1985
A/Pitle: Differential RNA splicing and post-translational cleavages in the human saliv
A,Accession: A25372

A. Accession: A2517.

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salivary proline-rich phosphoprotein precursor FRHI (allele FIF) - human cigencies: Homo sapiens (mine) aspense (mine) aspino) aspino) aspino) aspino aspino aspino aspino 
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N,Alternate names: salivary acidic proline-rich protein
C,Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic aid sequence not shown A;Molecule type: DNA A;Residues: 17-41, 'L', 43-118,'C',120-166 <AZE> A;Cross-references: BMBL:K03203 GGenetics: GGenetics: A;Gene GDB:PRH1 A;Cross-references: GDB:119515; OMIM:168730 A;Map position: 12p13.2-12p13.2 A;Introns: 22/1; 34/10 proline-rich protein C;Keywords: phosphoprotein; saliva; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity luv..
Best Local 7, Conservative
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               A; Molecule type: protein
A; Residues: 17-161, (0, 163-166 <8C3>
A; Residues: 17-161, (0, 163-166 <8C3>
A; Residues: 17-161, (0, 163-166 <8C3>
Blum, M.; Keller, P.J.
Biochemistry 30, 3351-3356, 1991
A; Reference number: A39355; MUD:91190884; PMID:1849422
A; Reference number: A39355; MUD:91190884; PMID:1849422
A; Reterence number: A39355; MUD:91190884; PMID:1849422
A; Residues: 123-166 < KAU>
A; Residues: 123-166 < KAU>
B; Rebinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
B; Robinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, C.; He non-glycosylated basic proline-ric
                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residudes: 123-166 (-1825)
R;Hay, D. L.; Bennick, A.; Schlesinger, D.H.; Minaguchi, K.; Madapallimattam, G.; Schluck
Biochem. J. 255, 15-21, 1989
A;Titler The primary structures of six human salivary acidic proline-rich proteins (PRP-
A;Reference number: S02562; MID:89061650; PMID:31968309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: protein
A,Residues: 123-166 <ROB>
C,Comment: The proposed biological functions are a highly potent inhibitor of crystal gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 47-71 <HA2>
R;Schlesinger, D.H.; Hay, D.I.
R;Schlesinger, D.H.; Hay, D.I.
A;Title: Complete covalent structure of a proline-rich phosphoprotein, PRP-2, an inhibit A;Reference number: JP0106; MUID:86222916; PMID:3710693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (in mature form) #status experimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C'Superfamily: proline-rich protein
C'Superfamily: proline-rich protein
C'Steyvords: calcium binding; phosphoprotein; pyroglutamic acid; saliva
E;1-16./Domain: signal sequence #status predicted <21G>
F;1-16./Product: protein C #status experimental <PRC>
F;17-16./Region: apartici A #status experimental <PRA>
F;17-46./Region: apartici mineral binding
F;17-71/Product: PRP-3 #status experimental <PRP>
F;123-166/Product: peptide P-C #status experimental <PRC>
F;17/Modified site: pyrolidone carboxylic acid (Gin) (in mature form)
F;24,38/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 42; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matchies 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:119516; OMIM:168790
A;Map postition: 12p13.2-12p13.2
A;Introns: 22/1; 34/1
A;Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 PRPPRGR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 17-166 <HAY>
A;Accession: S02563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PRPPRGR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: JP0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S02564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: S06153
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A, Gene: GDB: PRH2

RESULT 2 B25372

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hypothetical protein APB1916 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Accession: 07259
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nitilotriacetate monooxygenase, component A Atu6084 [imported] - Agrobacterium tumefa.
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Finod, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCle; Karp, P.; Romero, P.; Zhang, S.
Fisher, P.; Romero, P.; Zhang, S.
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm
                                A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
A,Residues: 1-450 «KUR»
A,Cross-references: GB.AE008690; PIDN:AAL46320.1; PID:g17744106; GSPDB:GN00189
A,Experimental source: strain C58 (Dupont)
                                                                                                          Score 39; DB 2; Length 200;
Pred. No. 20;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.5%; Score 38; DB 2; Length 450; 85.7%; Pred. No. 62; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.1%; Score 37; DB 2; Length 123; 100.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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C, Superfamily: nitrilotriacetate monooxygenase
                                                                                                                          92.9%;
85.7%;
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                                                                                Query Match
Best Local Similarity 85.7*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.73
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                13 PKPPRGR 19
                                                                                                                                                                                                                                                                                                                     1 PRPPRGR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PRPPRGR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 PRPPRG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PRPPRG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: AB3238
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: AB3238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: Atu6084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: APE1916
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Cipecies: Mycobacterium tuberculosis
Cipecies: Mycobacterium tuberculosis
Cipate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
Cicacession: E70610
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MJD:98295987; PMID:9634230
A; Reference number: A70500; MJD:98295987; PMID:9634230
A; Residues: Drellminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-561 < COL>
A; Coss-references: GB:29377; GB:A1123456; NID:93261726; PIDN:CAB07817.1; PID:e311160; A; Genetics:
A; Genetics:
A; Genetics:
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 29-Aug-1997
C;Accession: A27307
R;Azen, E.A.; Kim, H.S.; Goodman, P.; Flynn, S.; Maeda, N.
Am. J. Hum. Genet. 41, 1035-1047, 1987
A;Title: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich pro
A;Reference number: A27307; MUID:88074309; PMID:3687941
A;Reference number: A27307; MUID:88074309; PMID:3687941
A;Recession: A27307
A;Molecule type: DMA
A;Residues: 1-171 <AZE>
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$55609

Whypothetical protein 13 - equine herpesvirus 2
Cispecies: equine herpesvirus 2
Rizelford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J.Mol. Biol. 249, 520-528, 1995
Airitle: The DNA sequence of equine herpesvirus 2.
Airitle: The DNA sequence of equine herpesvirus 2.
Airitle: S5594; MUID:95302501; PMID:7783207
Airitle: Preliminary; nucleic acid sequence not shown; translation not shown Airitle: The DNA and Airitle: The DNA and Airitle: Airit
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A;Cross-references: GB:UZ0824; NID:g695172; PIDN:AAC13802.1; PID:g695187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Rv1215c - Mycobacterium tuberculosis (strain H37RV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 42; DB 2; Length 171; Best Local Similarity 100.0%; Pred. No. 5.9; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:119515; OMIM:168730
A;Map postition: 12913.2-12p13.2
C;Superfamily: proline-rich protein
C;Keywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: K03203
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 PRPPRGR 129
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hypothetical protein (mutA 5' region) - Streptomyces cinnamonensis
CjSpecies: Streptomyces cinnamonensis
CjSpecies: Streptomyces cinnamonensis
CjAccession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 22-Oct-1999
CjAccession: D40595
RyBirch, A.; Lebiser, A.; Robinson, J.A.
Glacteriol. 175, 3511-3519, 1993
A;Title: Cloning, sequencing, and expression of the gene encoding methylmalonyl-coenzyn
A;Recence number: A40585; MUID: 93273720; PMID: 8099072
A;Accession: D40595
A;Status: preliminary
A;Mocleacule type: DNA
A;Residues: 1-237 cBIR>
A;Cross-references: GB:L10064; NID:g153364; PIDN:AAA03039.1; PID:g153365
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A;Residues: 1-401 <DAN>
A;Cross-references: EMBL:AF039712; PIDN:AAB96717.1; GSPDB:GN00019; CESP:F54D7.3
A;Experimental source: strain Bristol N2; clone F54D7
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C;Accession: T32737
S;Date, M.; Twyman, B.
S;Dante, M.; Twyman, B.
A;Description: The sequence of C. elegans cosmid F54D7.
A;Reference number: 221218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Arthrobacter sp.
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 18-Jun-1999
C;Accession: A24026
R;Roberts, A.N.; Hudson, G.S.; Brenner, S.
Gene 35, 259-270, 1985
A;Reference number: A24026; MUID:86006275; PMID:4043733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-340 <ROB>
A;Cross-references: GB:M11276; NID:g142203; PIDN:AAA22075.1; PID:g142204
C;Superfamily: rRNA dadmine-N6-)-methyltransferase
C;Keywords: antibiotic resistance
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88.1%; Score 37; DB 2; Length 237;

Best Local Similarity 100.0%; Pred. No. 50;

Matches 6; Conservative 0; Mismatches 0; Indels
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A;Introns: 47/2; 92/3; 184/3; 228/1; 342/2
C;Superfamily: oxytocin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 6; Conservative
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Ajecteus: Periminary
Ajecteus: DNA
Ajecteus: 1-151 <SIM>
Ajecteus: 1-151 <SIM>
Ajecteus: 1-151 <SIM>
Ajecteus: 1-151 <SIM
Briones, M.R.S.; Beano, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Alvarenga, R.; Alberone, E. Bueno, M.R.P.; Enderdo, L.E.A.; Carraro, D.M.; Marchina, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiger Chado, M.A.; Madelra, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.; Madelra, A.M.; Madelra, A.Y.; Menck, C.F., Marques, M.V.; Martins, E.M.; Rosa, A.J.; de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R.; Carraro, D.M.; Carraro, D.M.; Sawasak, C.Y.; Sawasak, C.Y.; Sawasak, C.Y.; Sawasak, C.Y.; Sawasak, C.Y.; Saulako, M.H.; Vallada, H.; Van Siuvs, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A.; Salveira, A.S.; A.R.; Salveira, A.S.; Verfore, A.L.; Z.A.; Salveira, A.S.; A.R.; Salveira, A.S.; Verfore, A.L.; Z.A.; Salveira, A.S.; A.R.; Salveira, A.S.; Salveira, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein XF2514 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Date: 18-Aug-2000
Ascession: H82546
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MuID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                             Cyaccession: Assession mecquence_revision 10-may-2001 #text_change 10-may-2001
CyAccession: Assessy
Cyaccession: Assessy
Cyanonymous, The C. elegans Sequencing Consortium.
Solence 282, 2012-2018, 1998
AyTitle: Genome sequence of the nematode C. elegans: a platform for investigating biolog
AyTitle: Genome sequence of the nematode C. elegans: a platform for investigating biolog
AyNote: Genome sequence of the nematode C. elegans, a platform for investigating biolog
AyNote: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele
AyNote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
AyAccession: A88637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:chr_IV; PIDN:AAC04452.1; PID:g2911887; GSPDB:GN00022; CESP:W09G12
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             protein W09G12.9 [imported] - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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Matches 6; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-137 <STO>
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gag polyprotein - human T-cell lymphotropic virus type 1

(Species: human T-cell lymphotropic virus type 1, HTLV-1

(Species: human T-cell lymphotropic virus type 1, HTLV-1

(Species: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 26-Aug-1999

(Species: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 26-Aug-1999

(Species: 506073

Notleic Acids Res. 17, 7988, 1989

A;Title: Nucleotide sequence of the core (gag) gene from HTLV-1 isolate MT-2.

A;Accession: 506073, MUID:90016893; PMID:2678008

A;Accession: 506073

A;Accession: 506073

A;Accession: 506073; MUID:90016893; PMID:2678008
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Similarity 100.0%; Pred. No. 86;
6; Conservative 0; Mismatches 0; Indels
Query Match

88.1%; Score 37; DB 1; Length 429;

Best Local Similarity 100.0%; Pred. No. 86;

Matches 6; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
Matches 6; Conserv
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NiContains: major core protein p19; major core protein p24; nucleic acid-binding protein C; Species: human T-cell lymphotropic virus type 1, HTLV-1
A; Note: host Homo sapiens (man)
C; Dacession: A28136
R; Malik, K.T.A.; Even, J.; Karpas, A.
J. Gen. virol. 69, 1695-1710, 1988
A; Title: Molecular cloning and complete nucleotide sequence of an adult T cell leukaemia A; Reference number: A92797; MUID: 68274318; PMID: 2899128
A; Accession: A28136
A; Accession: A28136
                                                                                                                                                                                                                                                                                                                                                                               A.Note: host Homo sapiens (man)
C.Date: 14-Nov-1983 #sequence revision 27-Nov-1985 #text_change 26-Apr-1996
C.Accession: B93954; A91315; Ā03943
R.Sesiki, M.; Hattori, S.; Hirayama, Y.; Yoshida, M.
Proc. Natl. Acad. Sci. U.S.A. 80, 3618-3622, 1983
A.Title: Human adult T-cell leukemia virus: complete nucleotide sequence of the provirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Rolecule type: DNA
A;Residues: 1-429 <SEL>
A;Experimental source: strain ATK
R;Copeland, T.D.; Oroszlan, S.; Kalyanaraman, V.S.; Sarngadharan, M.G.; Gallo, R.C.
FBS Lett. 162, 390-395, 1983
A;Title: Complete amino acid sequence of human T-cell leukemia virus structural protein A;Reference number: A91315; MUID:84029174; PMID:6313426
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A;Residues: 11429 <MAL>
A;Cross-references: GB:D13784; GB:D00294; NID:g221866; PIDN:BAA02929.1; PID:g221867
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2.1-130/Product: major core protein p19 #status predicted <P19>
F.131-344/Product: major core protein p24 #status predicted <P24>
F.345-429/Product: mucleic acid-binding protein p15 #status predicted <P15>
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                                                                                                                                                                                                                                                                                                                                          probable gag polyprotein - human T-cell lymphotropic virus type 1 c;Species: human T-cell lymphotropic virus type 1, HTLV-1
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A;Residues: 345-415,'T',417-429 <COP>
C;Comment: This protein is synthesized as a gag-pol polyprotein.
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                     Length 401;
                                                                          0; Indels
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                  DB 2;
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                  Score 37;
Pred. No.
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100.0%; Pre
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Best Local Similarity 100.0
                        Query Match
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                          streptomyce
                                                                                                                                                                                                                                                                                                                        09yeb2 aeropyrum r
P34501 caenorhabdi
                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                     6, 2004, 15:31:19 ; Search time 4.51402 Seconds (without alignments) 80.746 Million cell updates/sec
                                                                                                                                                                                                                                             Description
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042130 g
P46529 m
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Q9c0c2 |
P32239 |
P30796 |
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P22165
043390
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P03345
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P14077
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P79266
P51512
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P30552
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088054
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                          hits satisfying chosen parameters:
                                                                                                            141681 segs, 52070155 residues
                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                               2384 FAUMAN
2384 FAU
DPM1 MOUSE
DPM1 CRIGR
VMUS STRCM
BRMA ARTS3
GAG HTL1C
GAG HTL1C
GAG HTL1C
TABE HUMAN
GASR PRANA
GASR PRANA
GASR RAFT
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GASR RAFT
GASR CANFA
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RAT
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HALVO
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PK1 STRTO
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Maximum Match 100%
Listing first 45 summaries
                         protein search, using sw model
                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                     seq length: 0
seq length: 2000000000
                                                                US-10-009-709-10
                                                                                                                                                                                                                                             DB
                                                                                                                                                                                   SwissProt_42:*
                                                                                                                                                                                                                                             Length
                                                                            1 PRPPRGR 7
                                                                                          BLOSUM62
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                                                                                                                                                                                                                                                                             Total number of
                                                                                                                                                                                                                                                           Scoring table:
                                                                       Perfect score:
                                                                                                                                       Minimum DB
Maximum DB
                                                                                                                                                                                     Database :
                          OM protein
                                                                              Sequence:
                                                                                                             Searched:
                                       Run on:
                                                                                                                                                                                                                                                                               Result
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P55637 rhizobium s 092834 chlamydia p 082616 escherichia 081629 escherichia 081621 escherichia 081737 haemophius 08x922 salmonalius 08x927 yersinia pe 08436 chlamydia m 09pjw3 chlamydia m P17588 herpes simp	
Y4RD RHISN Y518—CHLPN RLUD—ECO57 RLUD—ECO56 RLUD—ECOLI RLUD—SALTY RLUD—YERPE Y13—CHLTR Y13—CHLTR Y13—CHLTR CD2_HORSE	
28888888888888888888888888888888888888	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	

ALIGNMENTS

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PRPC_HINAN

AC CHINAN

AC CHINAN
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MIM; 168710; -.
GO; GO:0005615; C:extracellular space; TAS.
Repeat; Parotid gland; Phosphorylation; Signal; Polymorphism;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                          Genew, HGNC:9366, PRH1.
Genew, HGNC:9367, PRH2.
MIM, 168730, -.
MIM, 168790, -.
                                                 human saliva.";
                                                                                                                   Azen E.A.;
                                                                       saliva.
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118 PRPPRGR 124
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                                                                                                                                                                                                                                                                                                                                             163
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17
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24
38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsuo M.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z384 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                MOD_RES
VARIANT
                                                                                                                                                                                                            RES
                                                                                                                                                                                                                                                                                                 VARIANT
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                                                                                                                                                                                      MOD_RES
                                                                                                                                        DOMAIN
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                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schlesinger D.H., Hay D.I., "Complete primary structure of a proline-rich phosphoprotein (PRP-4), a potent inhibitor of calcium phosphate precipitation in human parotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the teeth.
-!- SUBCELLIULAR LOCATION: Secreted.
-!- PTM: Proteolytically Cleaved; PRP-2, PRP-1, and PIF-S yield PRP-4, PRP-3 (protein A), and PIF-F, respectively.
-!- POLYMORPHISM: Allele PRH1-4 is also known as PRH1 DA allele; allele PRH2-1 is also known as PRI or protein C; allele PRH2-3 is also known as PRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 123-166 (PEPTIDE P-C).
MEDLINE-80227634; PubMed=7390979;
Isemura S., Saitoh E., Sanada K.;
"The amino acid sequence of a salivary proline-rich peptide, P-C, and its relation to a salivary proline-rich phosphoprotein, protein C.";
Biochem. 87:1071-1077(1980).
                                                                                                                                                                                                                                                                                               MEDLINE=79173237; PubMed=438215;
Wong R.S.C., Hofmann T., Bennick A.;
"The complete primary structure of a proline-rich phosphoprotein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (In) Gross E., Melenhofer J. (eds.);
Septides: structure and biological function (Proceedings of the 6th
American peptide symposium), pp.133-136, Pierce Chemical Co.,
Rockford II. (1979).
"The primary structure of a salivary calcium-binding proline-rich phosphoprotein (protein C), a possible precursor of a related salivary protein A: 9/43-5948(1980).
                                                                                                                                                              Schlesinger D.H., Hay D.I., "Par B.I.," "Parimary structure of the active tryptic fragments of human and monkey salivary anionic proline-rich proteins."; Int. J. Pept. Procein Res. 17:34-41(1981)
                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 254:4800-4808(1979).
                                                                                                                    SEQUENCE OF 17-46 (PROTEIN C).
MEDLINE=81191179; PubMed=7228490;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 17-122 (PROTEIN A).
                                                                                                                                                                                                                                                                            SEQUENCE OF 17-122 (PROTEIN A)
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EMBL, K03203, AAA60184.1, -.
EMBL, M13057, AAA98807.1, -.
EMBL, M13058, AAA98608.1, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT PRH2-3 LYS-163.
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Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamaehita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Bugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Mashuo Y., Nagai K., Isogai T., Sugano S., Nagahari K., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDE P-C.
INHIBIT HYDROXYAPATITE FORMATION, BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08TF88, 015407, 08N938;

28-FFB-2003 (Rel. 41, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

210-OCT-2003 (Rel. 42, Last annotation update)

210-CT-2003 (Rel. 42, Last annotation update)

210-CT-2003 (Rel. 42, Last annotation update)

210-CT-2003 (Rel. 41, Last annotation update)

210-CAG repeat protein 1).

2NF384 OR NMP4 OR CAGHI.
                                                                                                                                                                                                                                                                                                      100.0%; Score 42; DB 1; Length 166; 100.0%; Pred. No. 2.4; ive 0; Mismatches 0; Indels
             SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2. SALIVARY ACIDIC PROLINE-RICH
                                                                                                                                PHOSPHORYLATION.
PHOSPHORYLATION.
PHOSPHORYLATION.
D - N (in allele PRH1-4).
FTId=VAR. 005563.
FTId=VAR. 005564.
O - K (in allele PRH2-3).
FTIG=VAR. 005564.
F - P (IN REF. 10).
W; ATDF6ZBF94E3G3EF CRC64;
                                                                                                      TO HYDROXYAPATITE AND CALCIT PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                        PHOSPHOPROTEIN 3/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                            41 41 F
166 AA; 17017 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 395-576 FROM N.A.
                                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                        166
46
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16
166
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-!- SIMILARITY: Contains 8 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lsoId=Q9EQJ4-2; Sequence=VSP_006921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9EQJ4-1; Sequence=Displayed;
                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSPAC; T05138; --
TRANSPAC; T05141; --
TRANSPAC; T05142; --
TRANSPAC; T05142; --
InterPro; IPR007087; Znf C2H2.
Pronom; PD000003; Znf C2H2; 8.
Prodom; PD000003; Znf C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB019281; BAA89664.1; -.
EMBL, AR216804; AAG40582.1; -.
EMBL, AF216805; AAG40583.1; -.
EMBL, AF216806; AAG40584.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, POB153; 1ZFD.
TRANSFAC; TO5136; -.
TRANSFAC; TO5137; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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      | InterProj | IPR00700s, | IPR00700s, | InterProj | IPR00700s, | IPR00700s, | IPR00700s, | IPR00700s, | IPR00003; 
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnth between the Swiss Institute. I here are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.cn/announce/or send an email to license@ibb-sib.ch).
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MEDLINE-20136045; PubMed=10669742;
Nakamoto T., Yamagata T., Sakai R., Ogawa S., Honda H., Ueno H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomí.
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                              Isoid=Q8TF68-2; Sequence=VSP 006920;
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2384_RAT STANDARD; PRT; 579 AA.
0SB024; 0SB012; 0SB013; QSUM15;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 384 (Nuclear matrix transcription factor 4)
CRS-associated zinc finger protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 1; Length 576; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 8 C2H2-type zinc fingers.
                           Event=Alternative splicing, Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                               Name=1;
IsoId=Q8TF68-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AK095734; BAC04618.1; -. EMBL; US0738; AAB91437.1; -. Genew; HGNC.11955; ZNF384. InterPro; IPR007087; Znf C2H2. Pfam; PF00096; zf-C2H2; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB070238; BAB85125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.9%;
   -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 PKPPRGR 194
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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AC 2384

AC 28-E

DT 28-E

DT 28-E

DT 10-C

DE Z1nC

CS RALI

CO MANN

CO MANN

CR SE

CO MANN

CR SE

CR SE
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-I. SUBGNIT: Interacts with Cas.
-I. SUBGNIT: Interacts with Cas.
-I. SUBGNIT: Interacts with Cas.
-I. ALTERNATIVE PRODUCTS:
Hirano N., Yazaki Y., Hirai H.;
"CIZ, a zinc finger protein that interacts with pl30cas and activates
"Ltb expression of matrix metalloproteinases.";
Mol. Cell. Biol. 20:1649-1658(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9EQJ4-3; Sequence=VSP 006922;
-!- TISSUE SPECIFICITY: Expressed in osteocytes, osteoblasts, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chondrocytes in bone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in ... /Fride YGP 006921.
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CONTRIBECT FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C77BL/6J; TISSUG=Cerebellum, Lung, and Small intestine;

KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KAWAI J., Shinagawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Radora K., Izawa M., Nishi K., Kiyosawa T., Saito R.,

Kadora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadora K., Matsudo T., Nikaido I., Pesole G., Quackenbush J.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Stzuki R., Tomita M., Wagner L., Washio T.,

Bake J., Deffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerte P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoro N.,

Sasaki H., Sator K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-cwa K., Wang K.H., Watz C., Whittaker C., Wilming L.,

Havsahizel R., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havsahizel R.,
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ID DPM1 MOUSE

AC 701652, Q90829;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DF 28-FEB-2003 (
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                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomita S., Inoue N., Maeda Y., Chishi K., Takeda J., Kinoshita T.; "A homologue of Saccharomyces cerevisiae Dpmip is not sufficient for synthesis of dolichol-phosphate-mannose in mammalian cells."; J. Biol. Chem. 273:9249-9254 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mannosylation of proteins.
-!- CATALYTIC ACTIVITY: GDP-mannose + dolichyl phosphate = GDP + dolichyl D-mannosyl phosphate.
-!- PATHRAY: Glycosylation.
-!- SUBCELLULAR LOCATION: Endoplasmic reticulum.
-!- SUBCELLULAR: Belongs to the glycosyltransferase family 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                           ٥;
                                                                                                                                                                      Score 39; DB 1; Length 579; Pred. No. 27;
                                                                                                                                                                                                                                       0; Indels
/FTId=vSP_006922.
GG -> RS_{IN REF. 1).
LA -> WP_{IN REF. 1}.
; FBC242E0D1050C45_CRC64;
                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98204925; PubMed=9535917;
                                    178 179 G
576 577 L
579 AA; 63139 MW;
                                                                                                                                                                  Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative 1
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                                    CONFLICT
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NA PEQUENCE FROM N.A.

NA PED L., SCOCKA J.R., Walker B.K., Wu J.S., Krag S.S.;

Pu L., SCOCKA J.R., Walker B.K., Wu J.S., Krag S.S.;

RIMLATION IN B4-2-1 CHO cells defective in MPD synthase activity.";

Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.

L. FUNCTION: Transfers mannose from GDP-mannose to Golichol

monophosphate to form dolichol phosphate mannose (Dol-P-Man) which

is the mannosylation of proteins (By similarity).

C. GATALTIC ACTIVITY: GDP-mannose + dolichyl phosphate = GDP +

dolichyl D-mannosylation.

C. GATALTIC ACTIVITY: GDP-mannose +

dolichyl D-mannosylation.

C. H. PATHWAY: Glycosylation.

C. H. SUBCELLULAR LOCATION: Endoplasmic reticulum (By similarity).

C. H. SUBCELLULAR LOCATION: Endoplasmic reticulum (By similarity).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Dolichol-phosphate mannosyltransferase (EC 2.4.1.83) (Dolichol-phosphate mannose synthase) (Dolichyl-phosphate beta-D-mannose synthase) (Dolichyl-phosphate beta-D-mannosyltransferase) (Mannose-P-dolichol synthase) (MPD synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                          EMBL; AB004789; BAA25759.1; -, EMBL; AK005268; BAB23920.1; -, EMBL; AK005484; BAB23602.1; -, EMBL; AK008548; BAB25702.1; -, EMBL; MCX08548; BAB25735.1; -, MCD; MGI.1330239; Dpml. GO; GO:000030; F:mannosyltransferase activity; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 17;
1; Mismatches
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Pfam; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF121895; AAD30975.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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14 PRPPQGR 20
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NCBL_TaxID=10029;
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ID DPM1_CF
AC Q9WU83;
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SEQUENCE FROM N.A.
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P03345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birch A., Leiser A., Robinson J.A.;
Cloning, sequencing, and expression of the gene encoding
methylmalonyl-coenzyme A mutase from Streptomyces cinnamonensis.";
J. Bacteriol. 175:3511-3519(1993).
                                                                                                                                                                             0;
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01-WAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
11-OCT-2003 (Rel. 42, Last amnotation update)
11-OCT-2003 (Rel. 48)
11-Machine N-6-methyltransferase (EC 2.1.1.48) (Macrolide-Inncosamide-streptogramin B resistance protein) (Erythromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae; Streptomycetaceae, Streptomyces.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Propionibacterineae; Nocardioidaceae; Aeromicrobium.
                                                                                                   90.5%; Score 38; DB 1; Length 266; 85.7%; Pred. No. 17; cive 1; Mismatches 0; Indels
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Transferase, Glycosyltransferase, Endoplasmic reticulum. SEQUENCE 266 AA; 29654 MW; 4AFB37EA3AC3329D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 25.0 kDa protein in mutA 5'region (ORF-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; D40595; D40595.
Hypothetical protein.
SEQUENCE 237 AA; 25025 MW; D9C55FED795AB455 CRC64;
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MEDLINE=93273720; Pubmed=8099072;
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MEDLINE=86006275; PubMed≈4043733;
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                                                          Query Match
Query Match
Best Local Similarity 85.,",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces cinnamonensis.
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Best Local Similarity 100.v
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                                                                                                                                                                                                                                                                                                      20 PRPPQGR 26
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AC DENAA_ARTS3
AC 01-MAR-1989
DT 01-MAR-1989
DT 01-MAR-1989
DT 10-CCT-2003
DE INCOSAMIGE-1
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GN ARTHODACTER
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OC NCBI TAXID=3
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RD | SEQUENCE FRO
REMAL MEDLINE=8600
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YMUS STRCM
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Roberts A.N., Hudson G.S., Brenner S.;
"An erythromycin-resistance gene from an erythromycin-producing
strain of Archrobacter sp.",
Gene 35:259-270(1985).
-! FONCTION: THIS PROFEIN PRODUCES A DIMETHYLATION OF THE ADENINE
RESIDED AT POSITION 2088 IN 238 RRNA, RESULTING IN REDUCED
APPLINITY BETWEEN RIBOSOMES & MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B
                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + rRNA = S-adenosyl-L-homocysteine + rRNA containing N(6)-methyladenine.
-!- SIMILARITY: Belongs to the rRNA adenine N-6-methyltransferase
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1-JUL-1986 (Rel. 01, Last seguence update)
10-OCT-2003 (Rel. 42, Last annotation update)
GAG polyprotein [Contains: Major core proteins P19 and P24; Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83221647; PubMed=6304725; Seiki M., Hartori S., Hirayama Y., Yoshida M.; Hartori S., Hirayama Y., Yoshida M.; Hartori B., Hirayama Y., Especial sequence of "Human adult T-cell leukemia virus; complete nucleotide sequence of the provirus genome integrated in leukemia cell DNA."; Proc. Natl. Acad. Sci. U.S.A. 80:3618-3622(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 131-155.

WEDLINE=82174882; PubMed=6280175;
WEDLINE=82174882; PubMed=6280175;
Oroszlan S. Sarngadharan M.G., Copeland T.D., Kalyanaraman V.S., Gilden R.V., Gallo R.C.;
Frinary structure analysis of the major internal protein p24 of human type C T-cell leukemia virus.";
Proc. Natl. Acad. Sci. U.S.A. 79:1291-1294(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-84029174; PubMed=6313426;
Copeland T.D., Oroszlan S., Kalyanaraman V.S., Sarngadharan M.G.,
Gallo R.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.1%; Score 37; DB 1; Length 340; 100.0%; Pred. No. 32; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human T-cell leukemia virus type I (strain ATK) (HTLV-I).
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBI_TaxID=11926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM06650; rADC; 1.
PROSITE; PS01131; RRNA_A_DIMETH; 1.
Antibictic resistance; Transferase; Methyltransferase.
SEOURNCE 340 AA; 37453 MW; E99A714C391952B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M11276; AAA22075.1; -.
IntecFro; IPR001737; RRNA A dimeth.
InterPro; IPR00051; SAM_Bind.
Pfam; PF00398; RrnaAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 345-429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 PRPPRG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PRPPRG 6
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6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395
                                                                                                                                                                                                    PIR; A28136; FOLJCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 PRPPRG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PRPPRG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAG HTL1M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZN FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P14077:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
GAG_HTL1M
    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPH THE PRESENCE OF THE PROPERTY OF THE PROPER
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-8824338; pubMed=2839128; MEDINE-8824338; pubMed=2839128; MAILX K.T.A., Even J., Karpas A.; "Molecular cloning and complete nucleotide sequence of an adult T cell leukaemia virus/human T cell leukaemia virus/human T cell leukaemia virus type I members of the ATLV/HTLV-I subgroup."; J. Gen. virol. 69:1695-1710(1988).
J. Gen. virol. 69:1695-1710(1988).
J. PTM. Specific enzymatic cleavages in vivo yield mature proteins.
J. PTM. Specific contains 2 CCRC-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
structural protein p15.";
PESS Lett. 162:390-395(1983).
-!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
-!- MISCELLANEOUS: This protein is synthesized as a Gag-Pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Major core proteins P19 and P24; Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human T-cell leukemia virus type I (Caribbean isolate) (HTLV-I).
Viruses, Retroid viruses; Retroviridae, Deltaretrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF0000; zf-CCHC; c. Pfam; PF00099; zf-CCHC; c. PRINYS; PR00939; Zf-CCHC; z. SMART; SM00343; ZnF C2HC; z. PROSITE; PS50158; ZF CCHC; z. PROSITE; PS50158; ZF CCHC; z. Core protein; Polyprotein; Zinc-finger; Repeat; 3D-structure. Core protein; Polyprotein; Zinc-finger; Repeat; 3D-structure. Care protein; polyprotein; Zinc-finger; Repeat; 3D-structure. Care protein; 2130 MAJOR CORE PROTEIN P19. MAJOR CORE PROTEIN P19. MAJOR CARE PROTEIN P15. MAJOR CALD-BINDING PROTEIN P15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> F (IN REF. 1; AAA96672).
03FFD4E5A4500284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                        polyprotein.
-!- SIMILARITY: Contains 2 CCHC-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCHC-TYPE 1.
CCHC-TYPE 2.
A -> T (IN REF. 2).
S -> F (IN REF. 1; AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               PLK; DSJOJE, CLEDON, DDB; 1QRJ; 26-SEP-01.
INTERPO; IPR003139; Gag p19.
INTERPO; IPR000721; Gag p24.
INTERPO; IPR008916; Retrov capsid C.
INTERPO; IPR008919; Retrov capsid C.
INTERPO; IPR001878; Znf CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47496 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                                                                                                                                                                                                                                              EMBL; J02029; AAA96672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02228; Gag_D19; 1.
Pfam; PF00607; Gag_D24; 1.
Pfam; PF00098; zf-CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 4
429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PRPPRG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses, Retroid v
NCBI_TaxID=11927,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PRPPRG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAG HTL1C
P14076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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-j- SIMILARITY: Contains 2 CCHC-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-07AN-1990 (Rel. 13, Created)
01-07AN-1990 (Rel. 13, Last sequence update)
01-0CT-2003 (Rel. 42, Last annotation update)
GAG polyprotein (Contains: Major core proteins P19 and P24; Nucleic acid-binding protein P15].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gray G.S., Bartman T., White M.; "Nucleotide sequence of the core (gag) gene from HTLV-1 isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEIC ACID-BINDING PROTEIN P15.
CCHC-TYPE 1.
CCHC-TYPE 2.
CPBF686497B738EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human T-cell leukemia virus type I (isolate MT-2) (HTLV-I).
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
Voll_TaxID=11928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.1%; Score 37; DB 1; Length 429; 100.0%; Pred. No. 41; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE ACLION FACUATION CARGING THE ACLION CARDING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 429 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 17:7998-7998(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=90016893; PubMed=2678008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 AA; 47514 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D13784; BAA02929.1; -.
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SMART;
SMART;
SMART;
                                                                                                                                                                                   RESULT 12
YMS5_CAEEL
ID YMS5_C
                                                                                                                 Matches
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                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crenarchaeon, Aeropyrum pernix Kl.";

DNA Res. 6:83-101(1999).

-!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
diphosphate + L-histidyl-tRNA(His).

-!- SUBCELDULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jûn-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H., Nomura N., Sako Y., Kikuchi H., Nomura N., Sako Y., Kikuchi H.,
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine-tRNA ligase)
                                                                                                                                                                                              .
0
                                                                                                                          NUCLEIC ACID-BINDING PROTEIN P15.
CCHC-TYPE 1.
CCHC-TYPE 2.
                                                                                                                                                                          Score 37; DB 1; Length 429;
Pred. No. 41;
                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                              Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
                                                                                                                                                        EF5201C934EF0291 CRC64;
                                                                                                                                                                                                                                                                                   438 AA
                                                                                                                                                                                  100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF 00127; -; 1.
InterPro; IPR004154; HGTP anticodon.
InterPro; IPR004516; HisS.
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K1;
MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP000060; BAA79634.1; -.
                                                                                                                                                         47584 MW;
                                                                                                                                                                             88.1%;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B72654; B72654.
                                                                                                                   131
345
355
378
378
429 AA;
                                                                                                                                                                                   Similarity 6; Conserva
                                                                                                                                                                                                                                    13 PRPPRG 18
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                 PRPPRG 6
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                      HISS OR APE0662
                                                                                                                                                                                                                                                                                   SYH AERPE
Q9YEB2;
                                                                                                                                                                          Query Match
Best Local S
                                                                                                                           CHAIN
ZN FING
ZN FING
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=Bristol N2;

WISDINE=94150718; PubMed=7906398; Separate C., Berks M.,

Wilson R., Annecough R., Anderson K., Baynes C., Berks M.,

Annecough R., Anderson K., Cooper J., Johnston L., Johnston L., Johnston L., Johnston L., Johnston L., Johnston L., Martiner B., Callaghan M.,

Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R., Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,

Naterston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,

Wohldman P.,
                                                                                                                 TIGREAMS; TIGRO0442; hisS; 1.
PROSITE; PS50862; AA TRNA LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                             Length 438;
                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                    438 AA; 49111 MW; ECCE67F59A9FB7BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein K03H1.5 in chromosome III.
K03H1.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1385 AA.
                                                                                                                                                                                                                                                                                                                88.1%; Score 37; DB 1
100.0%; Pred. No. 42;
iive 0; Mismatches
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR006195; tRNA ligase_II.
Pfam, PF03129; HGTP_anticodon; 1.
Pfam; PF00587; tRNA-synt_2b, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormPep, KO3H1.5, CE03459.
InterPro, IPR00553; AWDP.
InterPro, IPR003806; IPT.TIG.
InterPro, IPR003886; Nidogen ext.
InterPro, IPR00436; Sushi SCR_CCP.
InterPro, IPR001846; WWF_D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z29560; CAA82664.1; -. PIR; H88569; H88569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF03782; AMOP; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00094; vwd; 1.
                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00723; AMOP; 1.
SM00032; CCP; 1.
SM00429; IPT; 1.
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SEQUENCE 438 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- TISSUE SPECIFICITY: Detected in testis, ovary, lung, skeletal muscle, heart, prostate and pancreas, and at very low levels in brain and peripheral blood leukocytes.
-I- PTM: ADP-ribosylated by TNKS1 (in vitro).
-I- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in position 1071, 1097 and 1467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of long cDNA clones from human adult spleen. II. The complete sequences of 81 cDNA clones.", DNA Ref. 10:49-57(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=21082932; PubMed=11214970;
MEDLINE=21082932; PubMed=11214970;
Magase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
"Pagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIX.
The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB=Placenta, and Testis;
MEDLINE=21950796; PubMed=11854288;
Seimiya H., Smith S.;
"The telomeric poly(ADP-ribose) polymerase, tankyrase 1, contains multiple binding sites for telomeric repeat binding factor 1 (TRF1) and a novel acceptor, 182-kba tankyrase-binding protein (TAB182).";
J. Biol. Chem. 277:14116-14126(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Binds to the ANK repeat domain of TNKS1 and TNKS2.
-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Colocalizes with chromosomes during mitosis, and in the cytoplasm with cortical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jikuya H., Takano J., Kikuno R., Hirosawa M., Nagase T., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                   ö
                                                                             88.1%; Score 37; DB 1; Length 1385; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels
SMART; SM00539; NIDO; 1.
SMART; SM00216; VWD; 1.
Hypothetical protein.
SEQUENCE 1385 AA; 159181 NW; BDCD8F59CEA38C03 CRC64;
                                                                                                                                                                                                                                                              TABP HUMAN STANDARD; PRT; 1729 AA. 09C0C2.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
115-MAR-2004 (Rel. 41, Last annotation update)
128 kDa tankyrase 1-binding protein.
TNKS1BP1 OR TAB182 OR KIAA1741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Spleen;
MEDLINE=22579292; PubMed=12693554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  large proteins in vitro.";
Res. 7:347-355(2000).
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                                                                                Query Match 88.1
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                               1371 PRPPRG 1376
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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TABP_HUMAN
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ARG/GLU/LYS-RICH (CHARGED).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                             Marin, 20, G0:0005737; C:cytoplasm; NAS.
G0; G0:0005724; C:nuclear telomeric heterochromatin; NAS.
G0; G0:0005634; C:nucleus; NAS.
G0; G0:0005634; C:nucleus; NAS.
G0; G0:000506; F:ankyrin binding; NAS.
G0; G0:0007004; P:telomerase-dependent telomere maintenance; NAS.
InterPro; IRR008979; Gal bind like.
Nuclear protein; Chromosomal protein; ADP-ribosylation.
DOMAIN 2 ARG/GLU/LXS/PRO-RICH (CHARGED).
DOMAIN 127 767 PRO-RICH.
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15-WAR-2004 (Rel. 43, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
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Lee Y.-M., Beinborn M., McBride E.W., Lu M., Kolakowski L.F. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brain cholecystokinin-B/gastrin receptor. Cloning and
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Pred. No. 1.7e+02;
0; Mismatches 0; Indels
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S -> T (IN REF. 2).
C -> T (IN REF. 2).
C -> H (IN REF. 3).
F -> S (IN REF. 3).
F -> S (IN REF. 2).
W, C65F38FA37045C4A CRC64;
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                                                                                                                                                                                                                                                                                                                       GLY-RICH.
TANKYRASE-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 AA
EMBL; AF441771; AAM15531.1; -...
EMBL; AB051528; BAB21832.2; ALT_INIT.
BMBL; AK074113; BAB84939.1; ALT_FRAME.
GR; QSOCQ2; -...
MIM; G07104; -...
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100.0%; Pre
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01-OCT-1993 (Rel. 27, Last seq
15-MAR-2004 (Rel. 43, Last ann
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PRPPRG 70
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Best Local Similarity
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ID GASE HUMAN
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SEQUENCE FROM N.A. TISSUE=Placenta;

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P30796;
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R GO; GO:0004951; F:cholecystokinin receptor activity; TAS.

GO; GO:0004951; F:cholecystokinin receptor activity; TAS.

GO; GO:0004953; F:call surfaction; TAS.

GO; GO:0007166; P:call surface receptor linked signal transdu. .; TAS.

GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.

R GO; GO:0007586; P:digestion; TAS.

GO; GO:0007586; P:phosphatidylinositol-4,5-bisphosphate hydro. .; TAS.

GO; GO:0007202; P:phosphatidylinositol-4,5-bisphosphate hydro. .; TAS.

R GO; GO:000760; P:phosphatidylinositol-4,5-bisphosphate hydro. .; TAS.
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PROSITE; PSO37; G PROTEIN RECEP F1 1; 1.
PROSITE; PSO5262; G PROTEIN RECEP F1 2; 1.
PROSITE; PSO5262; G PROTEIN RECEP F1 2; 1.
PROSITE; PSO5062; G PROTEIN RECEP F1 2; 1.
PAIMITATE; POLYMOTPHISM; 3D-ETTUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;

Kopara S.A., Aronstam R.S., Sharma S.V.;

Kopara S.A., Aronstam R.S., Sharma S.V.;

Kopara S.A., Aronstam Proceins involved in signal transduction

sequenced by the Guthrie cDNA resource center (www.cdna.org).";

Submitted (UND-2003) to the EMBL/GenBank/DDB databases.

-I. FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B

receptors occur throughout the central nervous system where they

modulate anxiety, analgesia, arounsal, and neuroleptic activity.

This receptor mediates its action by association with G proteins

that activate a phosphatidylinositol-calcium second messenger
                                                "The human gastrin/cholecystokinin type B receptor gene: alternative splice donor site in exon 4 generates two variant mRNAs."; Proc. Natl. Acad. Sci. U.S.A. 90:9085-9089(1993),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SÜBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                     TISSUE=Brain;
MDDLINE=3352567; PubMed=8349705;
ILO M., Matsui T., Taniguchi T., Tsukamoto T., Murayama T., Arima
Nakata H., Chiba T., Chihara K.;
Functional characterization of a human brain cholecystokinin-B
receptor. A trophic effect of cholecystokinin and gastrin.";
J Biol. Chem. 269:18300-18305(1993).
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUB-Temporal cortex; TISSUB-Temporal cortex; Tate S.N., Gray J., Denyer J., Stolz M., Foord S., Lee M.G.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
MEDLINE-94022320; PubMed-8415658;
Song I., Brown D.R., Wiltshire R.N., Gantz I., Trent J.M.,
Yamada T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L08112; AAA35657.1; --
EMBL; L04473; AAA35660.1; --
BMBL; L10822; AAC37228.1; --
EMBL; D13305; BAA02564.1; --
EMBL; L07746; AAA91831.1; --
EMBL; AY322551; AAP84364.1; --
PIR; A47430; A47430.
PDB; 1L4T; 28-07A-03.
                                                                                                                     SEQUENCE FROM N.A.
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NREALTHE=92412082; PubMed=1530611;
Nakata H., Matsul T., Ito M., Taniguchi T., Naribayashi Y., Arima N., Nakamura A., Kinoshita Y., Chihara K., Hosoda S., Chiba T.;
"Cloning and characterization of gastrin receptor from ECL carcinoid tumor of Mastomys nacalensis.";
"Cloning and characterization of gastrin receptor from ECL carcinoid tumor of Mastomys nacalensis.";
-1- FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B receptors occur throughout the central nervous system where they modulate anxiety, analgesia, arousal, and neuroleptic activity. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenget
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-!- TISSUE SPECIFICITY: Stomach and brain.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Praomys natalensis (African soft-furred rat) (Mastomys natalensis)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                            S-palmitoyl cysteine (By similarity)
L -> F (in dbSNP:1805000)
/FTId=VAR 014684.
                                                                                                                                                                                                                                            7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
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Pred. No. 62;
; Mismatches 1; Indels
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/FIIda-VAR 014685.
R -> H (In dbSNP:1805002).
/FIIda-VAR 014686.
R -> Q (In dbSNP:1805001).
/FIIda-VAR 014687.
A -> P (IN RRF: 5).
L -> V (IN RRF: 5).
                                                                                                                                             EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                      cytoplasmic (Potential).

(Potential).

(Potential).

EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
                                                                                           3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Similarity 85.7%;
6; Conservative 0
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125
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Best Local Similarity
Matches 6; Conserv
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111111122888
13122222223
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36
127
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us-10-009-709-10.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-palmitoyl cysteine (By similarity)
EF13BA8B5FAA857A CRC64;
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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PIR, JQ1614; JQ1614.

PIR, PRO00276; GPCR_Rhodpsn.
Pfam, PF00001; 7tm il 1.
PROSITE; PR00237; GPCRRHODOPSN.
PROSITE; PS0227; GPROTEIN RECEP F1 1; 1.
PROSITE; PS02626; G_PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate.
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85.7%; Score 36; DB 1; Length 450; 85.7%; Pred. No. 63; 1:ve 0; Mismatches 1; Indels Query Match
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Search completed: April 6, 2004, 16:08:00 Job time : 4.51402 secs

Ogpaki xylella fas Q8244 human t-lym Q91sn5 arabidopsis Q8n1w5 homo sapien Q7tne5 mus musculu Q44731 caenorhabdi

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Q96ru3 homo sapien Q8rzz7 oryza sativ Q96ie7 homo sapien Q13545 homo sapien

Q9qral human t-lym

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Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
NCBL_TaxID=1140;
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Tsinoremas N.F., Golden S.S.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U44761, AAA86647.1;
InterPro; IPR001064; Crystallin.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
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DT 01-W
DT 01-W
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OC Viruit
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MEDINE=9825987, PubMed=9634230;
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Horneby T., Jagels K., Krogh A., McLean J., Moule S., Hamlin N., Holroyd S.,
Horneby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitehead S., Squares R.,
"Deciphering the blology of Mycobacterium tuberculosis from the
Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Ochkosh;
STRAIN=CDC 1551 / Ochkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Bishai W.;
                                                                                                                                                                                                                                                                      Gaps
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  P0577B11.16.

Orgra sativa (japonica cultivar-group).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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01-0TD-2003 (TERMELTE) 04, Last annotation update)
Hypothetical protein (Diester hydrolase, putative).
RV1215C OR MTC1364.27C OR MT1253.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteriaes, Corynebacterineae; Mycobacteriaes, Mycobacterium.
NCBI_TAXID=1773;
                                                                                                 STRAIN-CV. Nipponhare;
Sasaki T., Matsumoto T., Katayose Y.;
Sasaki T., Matsumoto T., Katayose Y.;
Sasaki T., Matsumoto T., Katayose Y.;
Submitted (UUL-2002) to the EMBL/GenBank/DDBU databases.
Submitted (UUL-2002) to the EMBL/GenBank/DDBU databases.
INEL, APO05504; BAC57819.1; -.
InterPro; IPR005885; PPR.
Pfam, PF01555; PPR.
SEQUENCE 535 APR, 9.
SEQUENCE 535 AA; 58557 MW; C2712C4178582982 CRC64;
                                                                                                                                                                                                                                           100.0%; Score 42; DB 10; Length 535; 100.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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0
                                                                                                                                                                                                                                                                                                                                                                                      561 AA.
                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; E70610; E70610.
TIGR; MT1233; -
Tuberculis; RV-15c; -
GO; GO:0005634; C:nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z93777; CAB07817.1; -.
EMBL; AE007002; AAK45510.1; -.
                                                                                                                                                                                                                                                        100.08;
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    114 PRPPRGR 120
                                                                                                                                                                                                                                                                                                1 PRPPRGR 7
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                                                                                        SEQUENCE FROM N.A.
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Gaps
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0016787; F:DNA binding; IEA.
GO; GO:0008451; F:Rada-Pro aminopeptidase activity; IEA.
GO; GO:0008451; F:metabolism; IEA.
GO; GO:0008451; F:metabolism; IEA.
GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR00879; Gal bind like.
InterPro; IPR001005; Myb_DNA_binding.
InterPro; IPR0010075; Myb_DNA_binding.
ITGRPAMS; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al protein; Hydrolase; Complete proteome.
561 AA; 62610 MW; 6D2C3253F2D3598D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORF 13.
Equine herpesvirus type 2 (strain 86/87) (EHV-2).
Equine herpesviruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
NCBI_TaxID=82831;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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MEDLINE=22709107; Pubmed=12788972;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
10-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypochetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                 MEDLINE=95302501; PubMed=7783207;
Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
"The DNA sequence of equine herpesvirus 2.";
J. Mol. Biol. 249:520-528(1995).
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85.7%; Pred. No. 57;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 12; Length 200;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                 Telford E.R.K.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, U20224; AAC13802.1;
PIR, S55609; SSS609.
                                                                                                                                                                                                                                                                                                                                                                                                                                   22356 MW; CF3306CF3C0974B1 CRC64;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Best Local Similarity 85.70,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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PKPPRGR 195
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PKPPRGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                       200 AA;
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                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Q72722;
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RC TISSUE-Testis,

RX STELLNE-Testis,

RX STELLNE-Testis,

RX Strausberg R.L., Feingold E.A., Grouse I.H., Derge J.G.,

Rtausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jozeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jozeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jozeberg B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Rahe J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RATSWINSKI M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Tones S.J., Marra M.R.,

R. Tones S.J., Marra M.R.,

R. Tones S.J., Marra M.R.,

R. Tones C.D., Sheven C.D., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Monting M., Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Monting M., Butterfield Y.S.,

R. Monting M., Marra M.R.,

R. Tones S.J., Marra M.R.,

R. Tones S.J., Marra M.R.,

R. Tones S.J., Marra M.R.,

R. Tones C.D., Sheven C.D., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Monting M. Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Monting M. Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Monting M. Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Monting M. Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Monting M. Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Monting M. Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Monting M. Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Monting M. Madan A., Schmutz J
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the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration of 60,770 full-length cDNAs.,
Nature 420:563-573(2002).
Nature 420:563-573(2002).
EMBL; AK086185: BAC39626.1; -.
PIR; PT0649; PT0712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.9%; Score 39; DB 4; Length 460; 85.7%; Pred. No. 65;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R., Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC083361; AAHS3861.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al protein. 460 AA; 50409 MW; 0C01860AFC3C71F2 CRC64;
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InterPro; IPR007087; Znf C2H2
PROSITE; PS00028; ZINC FINGER C2H2 1; 1.
PROSITE; PS50157; ZINC FINGER C2H2 2; 1.
SEQUENCE 517 AA; 55137 MW; 437@A6D9895D9ABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse cDNA sequences."; c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 PKPPRGR 139
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                                                                                                   SEQUENCE FROM N.A.
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                                           NCBI_TaxID=9606;
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SEQUENCE 46
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Matches
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READER SERVICE SER
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RESULT 10
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                                                                                    SOW NEW TENT TO THE CONTROL OF THE C
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MEDLINE-21608550; PubMed=11743193;
MEDLINE-21608550; PubMed=11743193;
MEDLINE-21608550; PubMed=11743193;
Med D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Medra V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Medra P., Clendenning J., Deatherage G., Giller W., Grant C.,
A. Kutyavin T., Levy R., Li M.-J., McCelland E., Palmieri A.,
Raymond C., Yoo H., Tao, Y., Biddle P., Jung M., Ferspan W., Perry M.,
A. Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
A. Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
M. Nester B.W.;
M. "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=1806951; PubMed=11743194; Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard C., Mullin L., Qurollo B., Gordon J., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowll C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; Gurson J., Lomo C., Sear C., Strub G., Gelo C., Slater S.; Gurson sequence of the plant pathogen and biotechnology agent Science 294:2132-2128(2001).
                                                         Gaps
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Score 39; DB 11; Length 517; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:000335; F:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR001865; Ribosomal 22.
                                                         Indels
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MONOOXYGENASe; Plasmid; CompleTe proteome.
SEQUENCE 450 AA; 50163 MW; D3ADB8261D68C026 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agrobacterium Tumefaciens (strain C58 / ATCC 33970).
                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nitrilotriacetate monooxygenase, component A.
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                                                                                                                                                                                                                                                                                                                    450 AA
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                    PRT;
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      92.9%;
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Best Local Similarity 85.7
Matches 6; Conservative
      Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                  Q8U651;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                         189 PKPPRGR 195
                                                                                                                  1 PRPPRGR 7
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Gaps

206 PRPPQGR 212

1 PRPPRGR 7

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Nagase T., Kikuno, R., Nakayama M., Hirosawa M., Ohara O., "Prediction of the coding sequences of unidentified human genes. XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proceins in vitro.";

DNA Res. 7:273-281(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUEBREAIN, and Thymocytes;
MEDLINE-21100880; PubMed=11161801;
Hicar M.D., Liu Y., Allen C.E., Wu L.C.;
"Structure of the Human Zinc Finger Protein HIVEP3: Molecular Cloning,
Expression, Exon-Intron Structure, and Comparison with Paralogous
Genes HIVEP1 and HIVEP2.";
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GO; GO: 0005634; C:nucleus; NAS.
GO; GO: 0003700; F: transcription factor activity; TAS.
GO; GO: 0003700; F: transcription of transcription, DNA-dependent; TAS.
InterPro; IPR002034; AIPM/Hcit_synth.
InterPro; IPR0034; AIPM/Hcit_synth.
InterPro; IPR0035; zf C2H2; 5.
SWART; SMART; ROUGSE; AIPM HOMOCIT_SYNTH_1; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 5.
Metal-binding; Zinc; Zinc, Z
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Kappa B and V(D)J recombination signal sequences binding protein.
KRC.
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01-UTN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
Hypothetical protein KIAA1555 (Fragment).
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PRT; 2406 AA.
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GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0008152; P:metabolism; IBA.
                                                                                                          (TremBirel, 17, Created)
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EMBL; AF278765; AAK01082.1; -.
HSSP; P15822; 18BO.
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            PRELIMINARY;
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2316 PRPPQGR 2322
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Best Local Similarity
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                                                                     Q9BZS0;
01-JUN-2001
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Q9HCL7
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STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
MEDLINE=970000351; PubMed=8843436;
Kadenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Thyroid,
MEDLINE=2042104; PubMed=10864405;
Pichon B., Mercan D., Pouillon V., Christophe-Hobertus C.,
Christophe D.;
"A method for the large-scale cloning of nuclear proteins and nuclear targeting sequences on a functional basis.";
EMBL; Biochem. 284:231-23(2000).
EMBL; AJ388548; CRB46847.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOT-1999 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLRel. 25, Last annotation update)
Hypothetical protein (Fragment).
Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; Nature 417:141-147(2002).
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larity 85.7%; Pred. No. 40;
Conservative 0; Mismatches 1: Indels
                                                                                                                                       STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                 Seeger K.J., Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA; 13226 MW; 0C8F1151DD942D4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL939115; CAB89457.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008819; F:ammonium transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001905; Ammonium transpt.
Pfam; PF00909; Ammonium transpt.
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STRAIN=A3(2) / M145;
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Matches 6; Conserv
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        STRAIN=A3 (2);
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Q9XSS0
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MEDLINE=593306146; PubMed=7786587;
Major M., Daenke S., Nightingale S., Desselberger U.;
"Differential Tax expression in HTLV type I-infected asymptomatic
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                              90.5%; Score 38; DB 4; Length 2414; 85.7%; Pred. No. 4.5e+02; tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                           2414 AA; 260294 MW; 05215E33CCEE2B65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human T-lymphotropic virus 1.
Viruses, Retroid viruses, Retroviridae, Deltaretrovirus.
NCBI_TaxID=11908,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carriers.";

Albs Res. Hum. Retroviruses 11:415-421(1995).

EMBL, $78309; ABB34666.2; BMBL, $78306; ABB34666.2; JOINED.

GO, GO:0019013; C:viral nucleocapeid; IEA.

InterPro; IPR003139; Gag_p19.

Pfam; PF02228; Gag_p19; I.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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InterPro; IPR002034; AIPM/Hcit_synth.
InterPro; IPR007087; Znf C2H2.
Pfan; PF00096; zf-C2H2; 5.
SWART; SM00355; ZnF C2H2; 5.
PROSITE; PS00815; AIPM HOMOCIT_SYNTH 1; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_1; 4.
Hypothetical protein.
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Best Local Similarity 85.7-
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Q86918;
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29 KZ63
10 90 KZ6
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88.1%; Score 37; DB 17; Length 123;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                       Score 37; DB 6; Length 118; Pred. No. 40;
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Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
NCBI_TaxID=56636;
                                                                                 118 AA, 12234 MW; A3DF7EC35748189C CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE1916.
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100.0%; Pred. No. ...
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STRAIN=K1;
MEDLINE=99310339; PubMed=10382966;
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Best Local Similarity 100.0
Matches 6; Conservative
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Hypothetical protein.
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SEQUENCE 118 AA; 1
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Search completed: April 6, 2004, 16:14:42 Job time : 25.3947 secs

31 PRPPRG 36

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GenCore version 5.1.6
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Searched:	1586107 seqs, 282547505 residues

1586107 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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11: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004ss:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		ΔH	AAB48780	AAB48779 \	AAB48778)	AAB48777	AAB48783	ABM65798	ABG18278	ABB38848	AAM32323	AAM72058	AAM59494	ABG53742	ABG41873	AAU65747	ABM62266	ABR57423	ABR56769	ADA83798	ADC98216	ABG26281	ABG03818	ADE07941	ABG70853	ABP76681	AA001213
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AA005792	ADC37585	AAU40822	ABM37341	AAU40575	ABM37094	ABP69375	ABB82733	AAR06875	AAY99907	AAM19074	ABB38280	AAM31712	ABB23461	AAM71425	AAM58902	ABG53123	ABG41232	AAU67167	ABM63686	
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ALIGNMENTS

XX XX XX XX PR 11-MAY-2000; 2000WO-SE000930. XX PA (STRO,) STROEMBERG N. PA (JOHA/) JOHANSSON I. XX XX XX PA (JOHA/) JOHANSSON I. XX		XX PN WO200069890-A1.	XX OS Homo sapiens.	XX KW Human; PRP-1; proline-rich protein; saliva; dental caries; KW chromosome 12p13.2; arginine catabolism; ammonia production; pH increase; KW oral bacterium; caries prevention.	XX DE Human saliva PRP-1 fragment (residues 102-108), SEQ ID NO:10.	XX DT 09-MAR-2001 (first entry)	AA AAB48780;	RESULT 1 AAB48780 ID AAB48780 standard; peptide; 7 AA.	
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New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.

Claim 4; Page 24; 36pp; English.

The invention relates to human PRP-1-derived oligopeptides (AAB48771-AB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12013.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide transmers. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-tich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-

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RESULT 2 AAB48779

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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia the catabolism of arginine. The peptides of the invention, being argininetich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-derived oligopeptides of the invention
                                                                                                                                                                                                                          Human, PRP-1; proline-rich protein, saliva, dental caries, chromosome 12p13.2; arginine catabolism, ammonia production; pH increase, oral bacterium, caries prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.
                                                                                                                                                                                  Human saliva PRP-1 fragment (residues 100-108), SEQ ID NO:8.
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                                                      AAB48778 standard; peptide; 9 AA.
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                                                                                                                                               09-MAR-2001 (first entry)
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JOHA/) JOHANSSON I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-1999;
                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                    AAB48778;
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                  RESULT 3
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                                       AAB48778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, PRP-1, proline-rich protein, saliva, dental caries,
chromosome 12p13.2; arginine catabolism, ammonia production, pH increase,
oral bacterium, caries prevention.
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                                                                               Query Match 100.0%; Score 42; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 7; Conservative 0; Mismatches 0; Indels
derived oligopeptides of the invention
                                                                                                                                                                                                                                                                                                                                 AAB48779 standard; peptide; 8 AA.
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Best Local Similarity 100.
Matches 7; Conservative
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                                            Sequence 7 AA;
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Length 9; Indels m

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, PRP-1, proline-rich protein; saliva; dental caries;
chromosome 12p13.2; arginine catabolism; ammonia production; pH increase;
oral bacterium; caries prevention.
chromosome 12p13.2; arginine catabolism; ammonia production; pH increase; oral bacterium; caries prevention.
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100.0%; Pred. No. 5.6;
ive 0; Mismatches 0; Indels
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                                                                                                                                                             (STRO/) STROEMBERG N. (JOHA/) JOHANSSON I.
                                                                                                                                                                                                                           WPI; 2001-031923/04
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Best Local Similarity
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                                       Homo sapiens.
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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPS (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's succeptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the carabolism of arginine. The peptides of the invention being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-derived oligopeptides of the invention
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Jones R, Carter D;
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                                                                                                                                                                New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.
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Benson DR,
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100.0%; Pred. No. 8.8;
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Zhang Y, Wang S, Jen S, Lodes MJ, 1
Barth B, Vallieve-Douglass J;
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                                                                                                                                                                                                                                      Claim 2; Page 24; 36pp; English.
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                                                                                   Johansson
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                  (STRO/) STROEMBERG N. (JOHA/) JOHANSSON I.
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                                                                                   Stroemberg N,
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Query Match
Best Local Similarity
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          Claim 7; SEQ ID NO 30474; 1481pp; English.
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23-AUG-2000; 2000US-00649167.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) are to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal cartivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other trails to assess blodiversity and to produce other types of dasorders or other trails to assess blodiversity and can be premised and products dependent on DNA and and to produce other types of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                    Claim 20; SEQ ID NO 48637; 103pp; English.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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27-SEP-2000; 2000US-0236359P
04-OCT-2000; 2000GB-00024263.
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing
Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAIS7546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #6360 encoded by probe for measuring placental gene expression.
                                             Claim 27; SEQ ID NO 31483; 639pp + Sequence Listing; English
                                                                                                                                                                                                                                                   100.0%; Score 42; DB 4; Length 132; 100.0%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe; microarray; human; placenta; antenatal diagnosis;
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                                                                                                                                                                                                                                                                                     0; Mismatches
                    gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                AAM32323 standard; protein; 132 AA.
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                                                                                                      Conservative
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tes 7; Conserv
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM32323;
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                                                                                                                                                                                                                                                                                                                                                     84
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                            Gaps
                                                                                                                                                                                                                                                                     Human, bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                          Human bone marrow expressed probe encoded protein SEQ ID NO: 32364.
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Length 132
                            Mismatches
 100.0%; Score 42;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM59494 standard; protein; 132 AA.
                                                                                                                                                          AAM72058 standard; protein; 132 AA.
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30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312P
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                                                                                                                                                                                                                (first entry)
                            7; Conservative
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                                                                                   84 PRPPRGR 90
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 Query Match
Best Local Similarity
Matches 7; Conserv
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                                                         1 PRPPRGR
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                                                                                                                                                                                                                                                                                                                                              WO200157276-A2.
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                               RESULT 10
AAM72058
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30-JAN-2001; 2001WO-US000664.

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzhahmer's disease, multiple scierosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                      Human, brain expressed exon, gene expression analysis, probe, microarray, Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy, cancer.
                                                            Human brain expressed single exon probe encoded protein SEQ ID NO: 31599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 31599; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 42; DB 4; Length 132; 100.0%; Pred. No. 51; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MXY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468FP.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
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05-NOV-2001 (first entry)
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Best Local Similarity luv...
7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483446/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 132 AA;
                                                                                                                                                                                                                                                                           WO200157275-A2.
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification for complements fragments). The probe hybridies at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperipprotecinaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at Etp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, single exon probe, asthma; lung cancer, COPD, ILD, chronic obstructive pulmonary disease, interstital lung disease, familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis, gaucher's disease; tuberous sclerosis, gaucher's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 42; DB 4; Length 132; 100.0%; Pred. No. 51; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID NO 32390; 658pp; English.
                                                                                                                                                                                                                               Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG41873 standard; peptide; 132 AA.
                               04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000US-023639P.
                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
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Best Local Similarity 10v...
7; Conservative
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AAU65747 standard; protein; 141 AA.

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Complete acid probes for measuring gene expression in a sample derived from human lung comprising single exon mucleic acid probes having of the human lung comprising single exon mucleic acid probes having one of 12614 mucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes or the novel set of probes which hybridise at high stringency to a mucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array; identifying exons in a elkaryotic genome, comprising (a) array; identifying exons in a elkaryotic genome, comprising (a) array; identifying exons in a elkaryotic genome, comprising (a) array; identifying at last one exon from genomic sequences of the exkaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung marsh, the probe is included in the above mentioned microarray; assigning exons in the above and (b) measuring the expression of each of the exons in several its the exons should be assigned to a single gene, a single exon for exon microarrays should be assigned to a single gene, a peptide comprising on microarrays should be assigned to a single gene, a peptide comprising on analysis, and for identifying exons in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in dense particularly using human for the exons fundamental dense full mind dense sclerosis, gallenges (ILD), familial idiopathic pulmonary albenosidates; pulmonary alseases with a sarchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence is a pertide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                  Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 31538; 634pp; English.
                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
                                                                    26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
27-SEP-2000; 2000US-023468FP.
27-SEP-2000; 2000US-0236599.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
30-JAN-2001; 2001WO-US000665.
                                                                                                                                                                                                                                                                                                   Penn SG, Hanzel DK,
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100.0%; Score 42; DB 5; Length 132; 100.0%; Pred. No. 51; 0; Mismatches Query Match Best Local Similarity 100. Matches 7; Conservative

Gaps ; 0 0; Indels 1 PRPPRGR 7

84 PRPPRGR 90

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RESULT 14 AAU65747

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acnes in a patient comprises contacting a presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by charge linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was SAPHO syndrome, synovitis, acne, pustulosis; hypertosis, osteomyelitis uvekitis, endophthalmitis, bone, joint, central nervous system; ELISA, inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant. polypeptides and nucleic acids useful for diagnosing infections, especially useful for Propionibacterium acnes immunogenic protein #26643. Mitcham JL, Wang SS, Jen S, Carter D; Example 1; SEQ ID NO 26942; 1069pp; English. 100.0%; Score 42; DB 100.0%; Pred. No. 54; ive 0; Mismatches ftp.wipo.int/pub/published_pct_sequences 21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P. 20-APR-2001; 2001WO-US012865 Skeiky YAW, Persing DH, M L'maisonneuve J, Zhang Y, (first entry) Query Match Best Local Similarity 100. Propionibacterium acnes. Propionibacterium acnes vaccinating against and treating acne vulgaris. WPI; 2001-616774/71. (CORI-) CORIXA CORP. N-PSDB; AAS59689 1 PRPPRGR 17 PRPPRGR Sequence 141 AA; WO200181581-A2 27-FEB-2002 01-NOV-2001. g ò ö

Bhatia A;

RESULT 15 ABM62266

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Gaps ..

0; Indels

4; Length 141;

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ABM62266 standard; protein; 141 AA.
                                                                                                      Ouery Match
Best Local Similarity
Matches 7; Conserv
                       4-APR-2003.
   ABM62266;
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Search completed: April
Job time : 40.1869 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maisonneuve JL;
Jones R, Carte
                                                                                                                                                                                                      Propionibacterium acnes predicted ORF-encoded polypeptide #26942.
                                                                                                                                                                                                                                                                                              Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 26942; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitcham JL, Skeiky YAW, Persing DH,
Zhang Y, Wang S, Jen S, Lodes MJ,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-2001; 2001US-00978825.
                                                                                                   20-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-381789/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ACF64618.
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0; Gaps

Similarity 100.0%; Score 42; DB 6; Length 141; Similarity 100.0%; Pred. No. 54; 7; Conservative 0; Mismatches 0; Indels

||||||| 17 PRPPRGR 23

1 PRPPRGR 7

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us-10-009-709-10.rapb

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Sequence 80, Appl
Sequence 17, Appl
Sequence 178111,
Sequence 106, App
Sequence 106, App
Sequence 18759, App
Sequence 18159,
Sequence 1815, App
Sequence 1815, App
Sequence 191513,
Sequence 1824, App
Sequence 1824, App
Sequence 1824, App
Sequence 1824, App
Sequence 181513,
Sequence 1824, App
Sequence 191513,
Sequence 181513,
Sequence 181513, Applementation of Sequence 191513, Applementation of Sequence 181513, Applem
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                                                                                                                                                                                                                         April 6, 2004, 16:14:50; Search time 27.4766 Seconds (without alignments) 66.909 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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cgn2_6/prodata1/pubpaa/us07_PUBCOMB.pep:*

cgn2_6/prodata1/pubpaa/us06_PUB_PUB.pep:*

cgn2_6/prodata1/pubpaa/us06_PUBCOMB.pep:*

cgn2_6/prodata1/pubpaa/us06_PUBCOMB.pep:*

cgn2_6/prodata1/pubpaa/us08_PUBCOMB.pep:*

cgn2_6/prodata1/pubpaa/us108_PUBCOMB.pep:*

cgn2_6/prodata1/pubpaa/us106_PUBCOMB.pep:*

cgn2_6/prodata1/pubpaa/us106_PUBCOMB.pep:*

cgn2_6/prodata1/pubpaa/us106_PUBCOMB.pep:*

cgn2_6/prodata1/pubpaa/us106_PUBCOMB.pep:*

cgn2_6/prodata1/pubpaa/us106_PUBCOMB.pep:*

cgn2_6/prodata1/pubpaa/us108_PUB.pep:*

cgn2_6/prodata1/pubpaa/us108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-864-761-43644
4 US-10-157-031-80
5 US-10-084-846A-7
2 US-10-084-846A-7
2 US-10-424-599-178111
2 US-10-424-599-285411
4 US-10-008-524A-106
5 US-10-424-599-18579
US-10-424-599-151579
US-10-424-599-151579
US-10-424-599-151579
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US-10-425-114-52873
US-10-457-372-7
US-10-389-566-1429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1071772 seqs, 262633353 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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42
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                              OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                               Run on:
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	eduence	equence 2'	equence 59	4	eguence 6(Ñ	ģ	Ğ	~	9	Ļ,	ຄ	equence 93	Sequence 8	quence 47	equence 1	á	equence 4	308	equence 107	equence 29,	9	equence 132	78	equence 112	9 132	equence 3,	equence 3,	edneuce	Sequence 1, Appli
	US-10-425-114-6916	US-10-108-260A-273	US-10-425-114-59	US-10-425-114-4347	US-10-425-114-6042	US-10-369-493-502	US-09-827-822	US-10-157-031-	US-09-981-151A-7	US-09-981-151A	US-08-811-519A-	US-10-225-567A-	US-10-292-798-91	US-10-240-154-	US-09-993-844-4	US-10-424-599-1833	US-10-424-599-24897	US-10-425-114-4170	US-10-104-047-	US-10-156-761-107	US-09-443-745-2	US-10-157-031-1	US-10-225-567A-	US-10-417-820A-7	US-10-417-820A~	US-10-417-820A-13	US-10-127-940-	US-10-441-757-	US-10-1	US-10-441-757-
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ALIGNMENTS

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Sequence 223703, Application US/10424599
Sequence 23703, Application US/10424599
Publication No. US2004003172A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TTLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 223703
LENGTH: 72
LENGTH: 72
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Best Local Similarity 100.0%; Score 42; DB 12; Length 72;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
, OTHER INFORMATION: Clone ID: PAT_MRT3847_44033C.1.pep
US-10-424-599-223703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43644, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1||||||
27 PRPPRGR 33
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US-09-864-761-43644
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Sequence 80, Application US/10157031

Publication No. US2030108890A1

| Publication No. US2030108890A1
| GENERAL INFORMATION:
| APPLICANT: Baranova, A. V. |
| APPLICANT: Walkovsky, N. K. |
| APPLICANT: Krukovskya, L. L. |
| TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences |
| FILE REFERENCE: 2760-103 |
| CURRENT APPLICATION NUMBER: US/10/157,031 |
| CURRENT APPLICATION NUMBER: US/10/157,031 |
| CURRENT APPLICATION NUMBER: US/10/157,031 |
| CURRENT APPLICATION NOS: 415 |
| SOFTWARE: PatentIn version 3.1 |
| SENGTHARE: PatentIn version 3.1 |
| TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 42; DB 14; Length 166; Best Local Similarity 100.0%; Pred. No. 83; Matches 7; Conservative 0; Mismatches 0; Indels (
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Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-157-031-80
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        APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
IITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR IITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGALIGN: Homo sapiens
FEATURE:
CTHER INFORMATION: MAP TO ACO06518.17
COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
COTHER INFORMATION: EXPRESSED IN BEDIA MARKOW, SIGNAL = 0.7
COTHER INFORMATION: EXPRESSED IN BODE MARKOW, SIGNAL = 0.95
COTHER INFORMATION: EXPRESSED IN BADLT LIVER, SIGNAL = 0.95
COTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
COTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
COTHER INFORMATION: STREAM HIT: BF068785.1, EVALUE 1.00e-01
US-09-864-761-43644
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                                                                                                                                                                                                        THILE REPERSONE: Aconica-E-
CURRENT APPLICATION NUMBER: US/99/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PELICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-06-03

PRIOR PILING DATE: 2000-06-03

PRIOR APPLICATION NUMBER: US 60/23,359

PRIOR PILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRI
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Gaps

; 0

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OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 2. OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 42; DB 15; Length 19652; 100.0%; Pred. No. 4.9e+03; tive 0; Mismatches 0; Indels 0;
                                                      Sequence 178111, Application US/10424599; Publication No. US20040031072A1
CENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
Sequence 7, Application US/10094846A
Publication No. US20040006026A1
GENERAL INFORMATION:
APPLICANT: WEITNAUER, GABRIELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-424-599-178111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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RESULT 3 US-10-157-031-80

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US-U9-864-761-381-98
US-U9-864-761-381-98
Sequence 38759, Application US/09864761
Sequence 38759, Application US/09864761
Sequence 38759, Application US/09864761
Sequence 38759, Application Sharion
ShellCany: Sharion Sharion
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Gen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION NUMBER: US 60/180,312
PRIOR PELING DATE: 2000-06-26
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                             Sequence 106, Application US/10350719
; Sequence 106, Application US/10350719
; Publication No. US20030219726A1
; GENERAL INFORMATION:
; APPLICANT: DOCUBAY, JOHN
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLCOMA
; TITLE OF INVENTION: URBSS
; FILE REFERENCE: 18396/2162
; CURRENT PELING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US/10/350,719
; CURRENT FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 180
; SOFWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
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                                                                                                                Score 37; DB 14; Length 40;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
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88.1%; Score 37; DB 15;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1;
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; LENGTH: 40

; TYPE: PRT

; ORGANISM: Human papillomavirus type 30

US-10-008-524A-106
                                                                                                                        88.1%;
85.7%;
                                                                                                10 PRPPHGR 16
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US-10-350-719-106
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Sequence 285441, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Dants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

SEQ ID NOS: 285684

SEQ ID NOS: 285684
                          APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 178111
LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-008-524A-106

| Sequence 106, Application US/10008524A |
| Sequence 106, Application No. US20030175682A1 |
| Sequence 106, Application No. US20030175682A1 |
| GENERAL INPORMATION: UPROCEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA |
| TITLE OF INVENTION: URGES |
| TITLE OF INVENTION: UNGRES: US/10/008,524A |
| CURRENT APPLICATION UNGRES: 09/314,268 |
| PRIOR APPLICATION NUMBER: 09/314,268 |
| PRIOR PILING DATE: 1999-05-18 |
| NUMBER OF SEQ ID NOS: 179 |
| SEQ ID NO 106
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85.7%; Pred. No. 1.9e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          92.9%; Score 39; DB 12; Length 71; 85.7%; Pred. No. 1.1e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131850C.1.pep
US-10-424-599-178111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT3847_99782C.1.pep
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.9
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
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41 POPPRGR 47
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61 PRPPRGK 67
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US-10-424-599-285441
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Acai Sou Yihua
APPLICANT: Aca Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5222)8
CURRENT APPLICATION NUMBER: US/10/424,599
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (59)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (76)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Sequence 1824, Application US/09925300

Patent No. U520020151881A1

GENBEAL INPORMATION:

APPLICANT: Craig Sceen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT FILING DATE: 2001-08-10

PRIOR PLICATION NUMBER: 67/126/06/5988

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 1824

LENGHH: 95
              98.1%; Score 37; DB 12; Length 71;
100.0%; Pred. No. 2e+02;
cive 0; Mismatches 0; Indels
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                     Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-10-424-599-191513
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 151579
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.9

OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.5

US-09-864-761-38759
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-30
PRIOR PRIOR DATE: 2000-09-30
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_10789C.1.pep
US-10-424-599-151579
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Publication No. US20040031072A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity '
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ORGANISM: Glycine max
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US-10-424-599-151579
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APPLICANT: Monsento Technology, LLC
APPLICANT: Monsento Technology, LLC
APPLICANT: Laure, Cathy C
TITLE OF INVENTION: Nucleic, Acid Molecules Associated with Oil in Plants
TITLE OF INVENTION: Nucleic, Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900) D
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/395,301
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR PILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-26
NUMBER OF FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin version 3.2
SEQ ID NO 1429
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/457,372
FILING DATE: 10-Jun-2003
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/778,717
FILING DATE: 12-DEC-1996
APPLICATION NUMBER: US/08/778,717
FILING DATE: 12-DEC-1996
APPLICATION NUMBER: 28-DEC-1995
ATTORNEY AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REFERENCE/DOCKET NUMBER: 204-031-0
TELECOMMUNICATION INFORMATION:
TELEBHOUE: 703-413-3200
RELEYANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 209
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Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 88.1%; Score 37; DB 15; Length 20
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1429, Application US/10389566 Publication No. US20040025202A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thaliana US-10-389-566-1429
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US-10-389-566-1429
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; Sequence 52873, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Soreen, Serven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
; SEQ ID NOS: 73128
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EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR
EXPRESSING SAID DNA SEQUENCE
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 12; Length 131;
Pred. No. 3.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                        Query Match

88.1%; Score 37; DB 12; Length 96;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                      ) OTHER INFORMATION: Clone ID: PAT_MRT3847_14957C.1.pep
US-10-424-599-191513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Clone ID: LIB3060-015-E9_FLI.pep
US-10-425-114-52873
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ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: FUSED
                      CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 191513 LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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APPLICANT: UENO, EII'
NOBUYUKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 PRPPEGR 103
                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
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ORGANISM: Zea mays
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US-10-425-114-52873
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Appli
Sequence 11, Appl
Sequence 7, Appli
Sequence 17, Appli
Sequence 7, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Appli
Sequence 11, Appl
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Sequence 28, Appl
Sequence 20577, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                               April 6, 2004, 15:56:34; Search time 10.271 Seconds (without alignments) 35.185 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                      Issued Patents AA:*
1: /cdp12_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgp2_6/ptodata/2/iaa/5B_COMB.pep:*
4: /cgp2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgp2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgp2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
6: /cgp2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-29452
US-09-252-991A-29452
US-09-252-991A-29430
US-09-252-991A-29430
US-09-252-991A-29430
US-09-252-991A-29430
US-09-252-991A-20099
US-09-252-991A-21772
US-08-195-868-30
US-08-195-868-30
US-08-195-868-30
US-08-195-868-30
US-08-195-868-30
US-08-195-868-30
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US-08-195-13
US-08-195-13
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US-08-195-13
US-09-433-353-17
US-08-433-353-17
US-08-433-353-17
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US-09-433-353-17
US-09-433-353-17
US-09-433-353-17
US-09-433-353-17
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                                                                                                                                                                                                                                               389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                               Searched:
                                                                                  Run on:
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Sequence 2016.

SEQUENCE SEGUENT MACCO INTERNITOR. NUMBER: US 00/074,788

FILTING DETLIANTOR NUMBER: US 00/074,788

FRIOR FILING DATE: 1999-02.18

SERICATION NUMBER: US 00/094,180

SERICATION NUMBER: US 00/094,180

SERICATION DATE: 1999-02.18

SEQUENCE SEQUE
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Sequence 2172, Application US/09252991A

Sequence 2172, Application US/09252991A

Patent NO. 6551795

GENERAL INFORMATION:
APPLICANT: Marc. N. Rubenfield et al.
APPLICANT: Marc. N. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPERENCE: 107196-118
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MAIC O'RUbenfield et al.
APPLICANT: MAIC O'RUbenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-1136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20099
LENGTH: 155
                                    Sequence 106, Application US/09314268
; Sequence 106, Application US/09314268
; Patent No. 6346377
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: URBOVERS
; TITLE OF INVENTION: URBOVERS
; TITLE OF INVENTION: UNBOR: 13789/80902
; CURRENT APPLICATION NUMBER: US/09/314,268
; CURRENT FILING DATE: 1999-03-19
; CARENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 106
; LENGTH: 40
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67;
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Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels
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. Sequence 20099. Application US/09252991A
. Patent No. 6551795
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Human papillomavirus type 30
US-09-314-268-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
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Matches 6; Conservative
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US-09-252-991A-21772
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                                       US-09-314-268-106
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29332
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/0252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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85.7%; Pred. No. 1e+02;
iive 1; Mismatches 0; Indels
                                                                 Query Match 100.0%; Score 42; DB 4; Length 418; Best Local Similarity 100.0%; Pred. No. 29; Matches 7; Conservative 0; Mismatches 0; Indels
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
, ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29452
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Best Local Similarity 85.7
Matches 6, Conservative
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Best Local Similarity 100..
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US-09-252-991A-24480
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LENGTH: 559
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Gaps
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APPLICANT: KAVANAUGH MD, DAVID
APPLICANT: WILLIAMS MDFHD, LEMIS T.
TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
TITLE OF INVENTION: 5-PHOSPHATASES (SIPS)
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEB: CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: RECOMBINANT
PUBLICATION
AUTHORS: NOBUVEL FUJI ET AL,
TITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
TITLE: FROM SAID FUSED DNA SEQUENCE AND METHOD OF
TITLE: FROM SAID FUSED DNA SEQUENCE AND METHOD OF
TITLE: EXPRESSING SAID FUSED PROTEIN
RELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 209
                                                  SOFTWARES PATENT RECOGNISHING SOFTWARES PATENT RECOGNISHING SOFTWARES PATENT RECOGNISHING SOFTWARES PATENT SOFTWARE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
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CLASSIFICATION:
APPLICATION NUMBER: US/09/195,868
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30, Application US/09195868 Patent No. 6090621 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703-413-3000
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Matches 6; Conservative
                                OPERATING SYSTEM:
SOFTWARE: Patent1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4560 HOR CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 PRPPRG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PRPPRG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-09-195-868-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-778-717-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANTION:
APPLICANTION:
APPLICANTION:
APPLICANTION:
APPLICANTION:
AUCHEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APPLICATION:
APPLICATION NUMBER: US/09/252,991A
CURRENT PEPPLICATION NUMBER: US/09/252,991A
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 34430

LENGTH: 208
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APPLICANT: NOBUYUKI, FUUJI
APPLICANT: NOBUYUKI, FUUJI
APPLICANT: OKADA, MASHISA
TITLE OF INVENTION: FUSED DNA SEQUENCE, FUSED PROTEIN
TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR
TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 182;
77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON STATE: UA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Score 37; Pred. No.
PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32430, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08778717
Patent No. 6602689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                  88.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 PRPPEGR 139
                                                                                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 21772
LENGTH: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 PRPPRG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PRPPRGR 7
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Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PRPPRG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-252-991A-32430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-32430
                                                                                                                                                                                                                                                                                                                 JS-09-252-991A-2177
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                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Sequence 41, Application US/08483533
Sequence 41, Application US/08483533
Sequence 41, Application US/08483533
GENERAL INFORMATION:
APPLICANT: Chou, Joany
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSED: MAXSHAIL, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Macker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.1%; Score 37; DB 3; Length 226; Best Local Similarity 100.0%; Pred. No. 93; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Chicago
STRATE: United States of America
COUNTRY: United States of America
ZIP: G666-6402
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: EADABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: EADABLE FORM:
WEDIUM TYPE: Patentin Release #1.0, Version #1.25
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PREIGRATION NUMBER: US/08/483,533
FILING DATE: 0-7MAR-95
CLASSIPTCATION DATA:
PREIGRATION NUMBER: 08/419,653
FILING DATE: 11-APR-95
PRIOR APPLICATION DATA:
PREIGRATION NUMBER: 07/661,233
FILING DATE: 31-MAR-92
FILING DATE: 31-MAR-92
FILING DATE: 31-MAR-92
ATTORNEY AGABTINES: O7/661,233
FILING DATE: 31-MAR-92
ATTORNEY AGABTINES: O7/661,233
NAME: FIRESTONE, LEIGH H.
RECISTATION NUMBER: 36,831
REFERENCE DOCKET NUMBER: 1182.004
TELECOMMUNICATION INFORMATION:
TELEFONE: 510-923-2707
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28097/32742
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REGISTRATION NUMBER: 28,491
REFERENCE/COCKET NUMBER: 2809
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-195-868-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-483-533-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PRPPRG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PRPPRG 7
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Patent No. 6340673
Patent No. 6340677
APPLICANT: Roizman, Bernard
APPLICANT: Roizman, Bernard
APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
Query Match

88.1%; Score 37; DB 3; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.1%; Score 37; DB 4; Length 355; 100.0%; Pred. No. 1.4e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSED:

AND SESSION MAISON CONTROL OF STREET STATE: Illinois STATE: Illinois STATE: Illinois STATE: Illinois STATE: Illinois COUNTY: United States of America COUNTY: United States of America COMPUTER: Illinois STATE: Illinois STATE: Illinois COMPUTER: ELOPPY disk COMPUTER: EAD STATE: PLOPPY disk COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: DATE OF STATE: PACENTIN Release #1.0, Version #1.25 SOFTWARE: PACENTIN BATA: APPLICATION NUMBER: US/09/283,471A FILING DATE: 04-ARR.1999 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: PRING APPLICATION DATA: PRING APPLICATION DATA: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27373/32742A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
THOUGH 355 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 27.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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                                                                                                                                                                                                                                                 173 PRPPRG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 PRPPRG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                 1 PRPPRG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PRPPRG 6
                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-283-471A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-283-471A-41
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PCT-US91-06532-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
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RESULT 15
US-09-370-368-6
Sequence 6, Application US/09370368
Sequence 7. Application US/09370368
Patent No. 6258932
GENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDES THAT BLOCK VIRAL INFECTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
TITLE REFERENCE: TRIPEP.003A
CURRENT APPLICATION NUMBER: US/09/370,368
CURRENT FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FRASESEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.1%; Score 37; DB 3; Length 429; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Human T-Cell Lymphotrophic Virus Type 1 US-09-370-368-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 1; LA Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                      PRIOR AFFLIANCE, COLLABOR PELLING DATE: US 07/554, PILLING DATE: 18-JUL-1990
ATTORNEY INFORMATION:
NAME: HALEY Jr. James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 17,794
REPERENCE/DOCKET NUMBER: IAPS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0670
TELERAX: (212)715-0674
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGRIH: 429 annino acids
FERRAY: ANTHO ACTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; P:
Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 429 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 88.1
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-672-483-3
              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 PRPPRG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PRPPRG 6
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Sequence 3, Application US/07672483

Patent No. 5359029

GENERAL INFORMATION:
APPLICANT: LACROIX, Martial
APPLICANT: LACROIX, Martial
APPLICANT: LACROIX, Man
ITIED OF INVENTION: PREPTIDES AND ANALOGUES AND MIXTURES
ITIED OF INVENTION: VIRUSES
TITLE OF INVENTION: VIRUSES
TITLE OF INVENTION: VIRUSES
INVERSPONDENCES: 2
CORRESPONDENCE 15H & NEAVE
STREET: 875 Third Avenue
CITY: New York
STATE: New York
STATE: New York
STATE: New York
COUNTRY: USA
ITIE: 10022-6250
COMPUTER: Eloppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Elb PC-0005/M3-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses
TITLE OF INVENTION: Vaccines and Methods
NUMBER OF SEQUENCES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknall, O'Toole, Gerstein, Murray &
COUNTY: Chicago
STRATE: Illinois
CONMPTR: Use PC compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Roppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Roppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 19910910
COMPUTER PAPLICATION NUMBER: D'O'GOS
SOFTWARE: PAPLICATION NUMBER: 27373/8235
FILING DATE: 19910910
CLASSIFICATION NUMBER: 27373/8235
FELEROMUNICATION INFORMATION:
NAME: Gruber, Lewis S.
TELEPONET: 1312/346-5750
TELEPONET: 25-3856
INPORMATION FOR EQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FENCENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 355;
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Best Local Similarity 100.0%; Pred. No. 1.4
Matches 6; Conservative 0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/672,483
FILING DATE: 19910302
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TOPOLOGY: 1.1. OLDARM
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CLASSIFICATION: 435
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                                                                         April 6, 2004, 15:52:34; Search time 6.72897 Seconds (without alignments) 85.771 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                      283366 seqs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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S53490
T45886
AB3238
S51941
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S55609
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JN0609
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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35
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Match Length
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1: pirl:*
2: pir2:*
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B3AG55	D72579	C55224	H72598	B85092	A70913	A88637	E72699	D72670	H82546	T46341	T15991	A75036	T35964	A72646	872709
H	N	N	~	7	N	7	7	N	N	ď	(7)	N	N	N	N
108	123	128	129	132	137	137	143	150	151	168	170	178	179	192	198
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30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30
30	31	32	33	34	35	36	37	38	33	40	4.7	42	43	4	45

ALIGNMENTS

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	FINCE: * FINCE: * Fince: mroling-rich whoshborrotein precursor PRH2 [validated] - human
	NiAlternate names: salivary acidic proline-rich protein PRH2
	N.Oontalins: peptide P-C (basic proline-rich peptide 18-8b); proline-rich prosphoprocein C.species Homo sabiens (man)
	C.Date: 31-Mar-1981 #Sequence revision 12-Apr-1996 #text change 08-Dec-2000 C.Date: 31-Mar-1981 #Sequence revision 12-Apr-1995 #text change 08-Dec-2000 C.Date: 3040551 Apr-19954; Apr-19964; Apr-19966; Apr-1996
	R, Maeda, N.; Kim, H.S.; Azen, B.R.; Smithles, O.
	J. BIOI. CHEM. 200, ILLES-LILSO, 1903 A,Title: Differential RNA splicing and post-translational cleavages in the human salivar
	A, Reference number: A92492; MUID:85289325; PMID:2993301
	A; Molecule type: mRNA
	A; Kesiduss: 1-166 cMAZ. A; frose-references: (GB:K03202; NID:q190481; PIDN:AAA60183.1; PID:g190482
	Int. J. Popt. Protein Res. 17, 34-41, 1981
	A; Accession: A19803
	A; Molecule type: protein
	A) Residues: 17-46 < SCH>
	KjAzmi, M.S.; Maedd, N. I Bidl Chem 241 A712-6718 1986
	A, Title: Structures of two HaelII-type genes in the human salivary proline-rich protein
	A; Reference number: A57868; MUID:86196106; PMID:3009472
	A,Accession: B57868
	A; Moral cute type: DNA
	A; KeBlades 1 1-to 7-to-7- A: Cross references: GB: M13058; NID: q190513; PIDN: AAA98808.1; PID: g190514
	R;Wong, R.S.C.; Bennick, A.
	J. Biol. Chem. 255, 5943-5948, 1980
	A;TILLE: The Primary Structure of a Salivary carcumum profile. The processors a professors and the professor
	A. Contents: protein C
	A,Accession: A92277
	A;Motecule Cype: procent b.Posidner: 17-19, VV. 21-166 <won></won>
	A; Note: the amino-terminal 46 residues are involved with inhibiting hydroxyapatite forma
	R; Wong, R.S.C.; Hofmann, T.; Bennick, A.
	J. Blol. Chem. 254, 4800-48094, 1979 a. Blol. Chem. 254, 4800-48094, 1979 b. mitle. The complete primary structure of a proline-rich phosphoprotein from human sali
	7;
	A; Contents: protein A
	A;Accession: A92254
	A;MOLEGULE (1989: procedu. b. becidines 17-19, (N. 21-122 < WO2>
	in Peptides: Structure and Biological Function (Proc. Sixth Amer. Peptide Symp.), Gross,
	A.fittle: Complete primary structure of a proline-rich phosphoprocein (PKP-4), a potent 1
_	A/Reference number: 5.2.2.2.2

Molecule type: protein Residues: 17-166 <HAY> Accession: S02563 Molecule type: protein Residues: 47-71 <HA2>

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A; Molecule type: protein
A; Residues: 123-166 < KAU>
R; Robinson, R; Kauffman, D.L; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
Biochem. J. 263, 497-503, 1989
A; Title: Primary structure and possible origin of the non-glycosylated basic proline-ric
A; Reference number: S06153; MUID: 90088384; PMID: 2688632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: protein. Flynn, S.; Maeda, N. Faston, Flynn, S.; Maeda, N. Fastdon, B.A.; Kim, H.S.; Goodman, P.; Flynn, S.; Maeda, N. Faston, B.A.; Kim, H.S.; Goodman, P.S. Plynn, S.; Maeda, N. M. J. Hum. Genet. 41, 1035-1047, 1987

m. J. Hum. Genet. 41, 1035-1047, 1055-1047

m. J. Hum. Genet. 41, 1035-1047

m. J. Hum. Bart. 1058-1047

m. J. Hum. Genet. 41, 1035-1047

m. J. H
                         C;Species: Homo sapiens (man)
C;Date: 29-Aug-1987 #text change 20-Aug-1999
C;Accession: 525372; A57868; 502562; G38355; S06153; B27307
C;Accession: 525372; A57868; S02562; G38355; S06153; B27307
J; Biol: Chem. 260, 11129-11130, 1985
A;Title: Differential RNA splicing and post-translational cleavages in the human salivar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:K03203; NID:g190483; PIDN:AAA60184.1; PID:g190484
R;Kim, H.S.; Maeda, N.
Biol. Chem. 261, 6712-6718, 1986
A;Title: Structures of two HaeIII-type genes in the human salivary proline-rich protein A;Reference number: A57868; MUID:86196106; PMID:3009472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,Molecule type: DNA
,Residues: 1-166 <KLM>
,Cross-references: GB:W13057; NID:g190511; PIDN:AAA98807.1; PID:g190512
,Hay, D.1.; Bennick, A.; Schlesinger, D.H.; Minaguchi, K.; Madapallimattam, G.; Schluck
Lichem. J. 255, 15-21, 1988
,Title: The primary structures of six human salivary acidic proline-rich proteins (PRP-
,Reference number: S02562; MUID:89061650; PMID:3196309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Wolecule type: protein
A.Residues: 47-71 «HAY»
R.Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Biochemistry 30, 3351-3356, 1991
A.Pitle: Basic proline-rich proteins from human parotid saliva: relationships of
A.Reference number: A38355; MVID:91190884; PMID:1849422
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proline-rich phosphoprotein precursor PRH1 (allele PIF) - human
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N;Alternate names: salivary acidic proline-rich protein
C;Species: Homo sapiens (man)
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ilarity 100.0%; Pred. No. 17;
Conservative 0; Mismatches 0
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C;Keywords: phosphoprotein; saliva; tandem repeat
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Cross-references: EMBL:K03203
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A;Map position: 12p13.2-12p13.2
A;Introns: 22/1; 34/1
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A;Molecule type: DNA
A;Residues: 17-41,'L',43-118,'C',120-166 <
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ses 6; Conserv
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A; Residues: 1-166 < MAE>
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A;Amp position: 12p13.2-12p13.2
A;Introns: 22/1; 34/1
A;Introns: 22/1; 34/1
C;Superfamily: proline-rich protein
C;Reywords: calcium binding; phosphoprotein; pyroglutamic acid; saliva
C;Reywords: calcium binding; phosphoprotein | PRCS | P:1-16/Product: protein C #status experimental <PRC>
F;17-16/Product: protein A #status experimental <PRC>
F;17-122/Product: protein A #status experimental <PRC>
F;17-122/Product: pperion a patitic mineral binding
F;17-46/Region: apatitic mineral binding
F;17-16/Product: peptide experimental <PRC>
F;13-16/Product: peptide experimental <PRC>
F;13-16/Product: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F;24,38/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 123-166 <1SB>
R;Hay, D.I.; Bennick, A.; Schlesinger, D.H.; Minaguchi, K.; Madapallimattam, G.; Schluck
Biochem. J. 255, 15-21, 1988
A;Title: The primary structures of six human salivary acidic proline-rich proteins (PRP-A;Reference number: S02562; MUID:89061650; PMID:3196309
A;Accession: S02564
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;Residues: 123-166 <KAU>
;Robinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
;Robinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
;71tle: Primary structure and possible origin of the non-glycosylated basic proline-rid
;Reference number: S06153; WUID:90088384; PMID:2688632
                                                                                       A;Molecule type: protein
A;Residues: 17-122 <8C2>
A;Residues: 17-122 <8C2>
A;Note: the authors 2011 this protein PRP-4
A;Note: the author, E.; Sanada, K.
J. Biochem. 87, 1071-1077, 1980
A;Pittle: The amino acid sequence of a salivary proline-rich peptide, P-C, and its relations amino acid sequence of A;Pittle: The peptide P-C
A;Reterence number: A91954; MUID:80227634; PMID:7390979
A;Contents: peptide P-C
A;Accession: A91954
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tt. J. Pept. Protein Res. 27, 373-379, 1986
Title: Complete covalent structure of a proline-rich phosphoprotein, PRP-2, an inhibit
Reference number: JP0106; MUID:86222916; PMID:3710693
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Residues: 123-166 <ROB>
;Comment: The proposed biological functions are a highly potent inhibitor of crystal
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Residues: 17-161, Q', 162-166 <SC3>
Residues: 17-161, Q', 162-166 <SC3>
Rexperimental source: parotid gland
Revieman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Rauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Rauffman, D.L.; Bassio proteins from human parotid
Reference number: A38355; MUID:91190884; PMID:1849422
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Status: preliminary

cession: S06153

Gene: GDB:PRH2

119 RPPRGR 124

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RESULT 2 B25372

1 RPPRGR 6

Query Match Best Local Similarity Matches 6; Conserv

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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.S.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                          A,Cross-references: GB:Z93777; GB:AL123456; NID:g3261726; PIDN:CAB07817.1; PID:e311160;
A,Experimental source: strain H37Rv
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A;Residues: 1-784 «XUR»
A;Cross-references: GB:AE008688; PIDN:AAL42309.1; PID:g17739711; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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A;Molecule V:ppe: DNA
A;Residues: 1-794 <KUJR>
A;Ccross-references: GB:AE007869; PIDN:AAK87094.1; PID:g15156354; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AG2736
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                                                                                                                                                                                                    100.0%; Score 35; DB 2; Length 561; 100.0%; Pred. No. 51; ive 0; Mismatches 0; Indels
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C,Superfamily: virulence-associated protein vacB homolog
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A;Map position: circular chromosome
C;Superfamily: virulence-associated protein vacB homolog
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Best Local Similarity 100.0
Matches 6; Conservative
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              A; Residues: 1-561 <COL>
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C;Species: Ralobacterium sp. NRC-1
C;Species: Ralobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession. D84335
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T. T2176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
S;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 29-Aug-1997
2;Accession: A27307
3;Azen, B.A.; Kim, H.S.; Goodman, P.; Flynn, S.; Maeda, N.
4m. Genet. 41, 1035-1047, 1987
4;Title: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich profiterence number: A27307; MUID:88074309; PMID:3687941
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Daces: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 22-Oct-1999
C;Dacession: E70610
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Titler Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: E70610
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A;Cross-references: GB:AE004437; NID:g10581288; PIDN:AAG20048.1; GSPDB:GN00138
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A.Cross-references: GDB:119515; OMIM:168730
A.Map postition: 12p13.2-12p13.2
S.Superfamily: proline-rich protein
C.Keywords: phosphoprotein
                                                                                                                                                                                                A;Accession: A27307
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
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1/Cross-references: EMBL:K03203
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Best Local Similarity 100.v
Loca 6; Conservative
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probable adenylyl-sulfate kinase (EC 2.7.1.25) - Mycobacterium tuberculosis (strain H37F N.Alternate names: ATP sulfurylase large chain N.Alternate names: ATP sulfurylase large chain N.Contains: adenylylaulfate kinase (EC 2.7.1.25); sulfate adenylyltransferase (EC 2.7.7 C; Species: Mycobacterium tuberculosis C; Pate: 2: Thay-1999 #sequence_reviston 21-May-1999 #text_change 03-Jun-2002 C; Accession: B70772 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier T. Churcher C. ........
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A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, S.K.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Authors: Salzberg, S.D.; Schwarz, C.M.; Venter, J.C.; Davis, R.W.
A.Authors: Salzberg, C.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Authors: A.Authors: Askittl; MUID:21016719; PMID:11130712
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C,Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C; Reywords: BF hand
and the gene of the histidine-rich
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A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Tetle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; FMID:9634230
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2001
C:Accession: F96776
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.4%; Score 32; DB 2; Length 363; Best Local Similarity 83.3%; Pred. No. 1.2e+02; Matches 5; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                 A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-363 - KKIL>
A,Cross-references: GB:M28063; NID:g160330; PID:g951371
C,Superfamily: knob-associated histidine-rich protein
A;Title: Homologous sequences in Plasmodium cynomolgi a:
A;Reference number: A44971; MUID:90220761; PMID:2183051
A;Accession: C44971
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91.4%; Score 32; DB 2; I
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0;
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A; Residues: 1-541 <STO>
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Mcclell Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Atu0440 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
2,Species: Agrobacterium tumefaciens
2,Pate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dypothetical protein 13 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Species: 27-0ct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S55609
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J, Mol. Biol. 249, S20-528, 1995
A;Accession: S55609
A;Accession: Tolo A;Accession not shown
A;Accession: Accession National A;Accession not shown
A;Accession: Accession National A;Accession National A;Accession National A;Accession National A;Accession National A;Accession National National A;Accession National Na
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A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-167 <KUR>
A;Cross-references: GB:AE006688; PIDN:AAL41459.1; PID:g17738783; GSPDB:GN00186
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histidine-rich knob protein homolog KPRPC - Plasmodium cynomolgi (fragment)
C;Species: Plasmodium cynomolgi
C;Species: Plasmodium cynomolgi
C;Species: 14-May-1993 #sequence_revision 14-May-1993 #text_change 03-Nov-2000
C;Accession: C4971
R;Kilejian, A.; Yang, Y.F.; Cochrane, A.H.; Rashid, M.A.
Mol. Biochem. Parasitol. 38, 291-293, 1990
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91.4%; Score 32; DB 2; Length 167;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels
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14 KPPRGR 19
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511 KPPRGR 516
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C; Genetics
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A,Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyt A; Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description: as sulfate adenylyltransferase catalyzes the reaction of sulfate and ATP (Superfamily: nodulation protein nod0; adenylylsulfate kinase homology; translation eld (Keynords: GTP binding) multifunctional enzyme; nucleotide binding; nucleotidyltransfer (FL9/Romain: translation elongation factor Tu homology cETU> (11-18/Region: nucleotide-binding motif A (P-loop) (143-146/Region: GTP-binding NCM pentif (143-146/Region: GTP-binding NCM pentif (143-605/Domain: adenylylsulfate kinase homology cASK> (145-605/Domain: adenylylsulfate kinase homology cASK> (145-605/Domain: adenylylsulfate (1450-605/Domain: ade
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A;Residues: 1-669 <IZU>
A;Cross=references: DDBJ:D63850; NID:92558500; PIDN:BAA22896.1; PID:d1023766; PID:925589
Comment: This protein translocates to the nucleus and directly functions in mitogenic
F;1-93/Region: hath #status predicted
F;321-363/Region: nuclear location signal
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                                                                                                                                                                                        ,Gene: cysN
Note: contains domains equivalent to cysN and cysC
;Complex: may associate with small chain to form a sulfate activation complex with aden
;Function: <ASKF>
                                                                                                                                                                                                                                                                                                                                                        Description: as adenylylsulfate kinase catalyzes the phosphorylation of adenylylsulfat
Function: <SATE>
                                      Cross-references: GB:Z73419; GB:AL123456; NID:g3261573; PIDN:CAA97752.1; PID:g1322410
Experimental source: strain H37Rv
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A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81407.1; PID:g5106096
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: G72468
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Date: 17-Nov-1997 #sequence_revision 17-Nov-1997 #text_change 05-Nov-1999
Accession: JC5662
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2e+02;
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Pred. No. 2e+02
1; Mismatches
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83.3%;
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Best Local Similarity 83...
S; Conservative
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439 RPPRGK 444
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274 KPPRGR 279
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Matches 5; Conserv
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A) Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH C) Superfamily: GLGF domain homology; flavodoxin homology; NADPH-ferrihemoprotein reduct. (2 Keywords: calmodulin binding; chromoprotein; flavoprotein; heme; iron; metalloprotein F;23-95/Domain: GLGF domain bomology «GLG»
F;725-745/Region: calmodulin binding #status predicted F;755-1394/Domain: NADPH-ferrihemoprotein reductase homology «FLX»
F;881-912/Region: RADP binding #status predicted F;1027-1038,1170-1180/Region: FAD binding #status predicted F;1245-1253,1343-1358/Region: NADP binding #status predicted F;374/Binding site: phosphate (Ser) (covalent) #status predicted F;415/Binding site: heme iron (Cys) (axial ligand) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                  itric-oxide synthase (EC 1.14.13.39), neuronal - mouse
Species: Mus musculus (house mouse)
Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                      Gaps
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Cross-references: GB:D14552; NID:g397828; PIDN:BAA03415.1; PID:g408806
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                    probable membrane protein PAB2428
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                                                                                   Score 32; DB 2; Length 840;
Pred. No. 2.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: nucleic acid sequence not shown
A,Gene: APE2392
C,Superfamily: Pyrococcus abyssi
                                                                                          Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Matches 5, Conservative
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April 6, 2004, 15:51:34 ; Search time 21.7009 Seconds (without alignments) 87.236 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                            1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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    sp_archea:*
    sp_bacteria:*
    sp_tungi:*
    sp_human:*
    sp_nvertebrate:*
    sp_mammal:*
    sp_mammal:*
    sp_mic:*
    sp_organelle:*
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sp_virus:*
sp_vertebrate:*
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_rvirus:*
sp_bacteriap:*

rvirus:*

sp_archeap:*

		-	Description	Q82gy4 streptomyce	Q910j9 streptomyce	094b27 arabidopsis	O86639 streptomyce	Q82k61 streptomyce	Q54729 synechococc	Ospito xanthomonas	Q96In6 homo sapien	QBtxv0 methanopyru	Q9hp22 halobacteri	Q84sd0 oryza sativ	005316 mycobacteri	Q7u0d5 mycobacteri	Q8s103 oryza sativ	Q7y0d7 oryza sativ	
SUMMARIES			QH	Q82GY4	Q91.0J9	Q94B27	086639	Q82K61	Q54729	QBPITO	096LN6	QBTXVO	Q9HP22	Q84SD0	005316	Q700D5	088103	Q7Y0D7	Q8NBC6
			DB	16	16	10	16	16	(1	16	4	17	11	10	16	16	10	10	4
			Match Length DB	186	246	255	266	267	332	344	378	420	433	535	561	561	591	658	969
	æ	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	35	35	3	35	35	35	35	35	35	38	35	35	32	35	35	35
		Result	No.	1	63	m	4	Ŋ	ø	7	œ	σι	10	11	12	13	14	15	16

Best Local Similarity

Q9yq39 pseudorabie Q9yq39 pseudorabie Q9uffud agrobacteri Q92qmo rhizobium m Q7uxee rhodopiral Q8mze9 drosophila Q9ajp5 myxococus Q9ajp5 myxococus Q9ajp5 myxococus Q9ajp5 myxococus Q9bx6 homo agrien Q6619 equine herp Q96419 homo sapien Q96419 homo sapien Q9641 rattus norv Q722 homo sapien Q9641 rattus norv Q7272 homo sapien Q9642 homo sapien Q9649 homo sapien Q92xy rhizobium m Q964xy homo sapien Q964x9 myxobacteri Q3540 mus musculu Q954x16 mus musculu Q954x16 mus musculu Q964x16 mus musculu Q954x16 mus musculu Q954x16 mus musculu Q954x16 mus musculu Q954x17x17x17x17x17x17x17x17x17x17x17x17x17x	OHOL
Q9YQ39 Q9YQ39 Q9YQYQ0 QYUXXEE Q9ML73 Q9ML73 Q9ML73 Q9GYYU Q9EG19 Q9EG13	Q9BW08 Q7Z4VS
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ALIGNMENTS

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SEQUENCE FROW N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-22608306; PubMed=12692562;
MEDLINE-22608306; PubMed=12692562;
SAKAKI Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganisms Streaptomyces avermitilis.";
NAL. Biotechnol. 21:526-531(2003).
EMBL; AP005036; BAC71474.1; ---
Hypothetical protein; Complete protecome.
SEQUENCE 186 AA; 20723 MW; 89128D7AC3CDBOCI CRC64;
                                                                                                                                                                                                                                                          STRAIN-MA-4600/ ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-214747403; PubMed=11572948;
Omura S., Ikeda H., Ishlakawa J., Hanmoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 35; DB 16; Length 186; 100.0%; Pred. No. 37;
                                                                                                                                                               Streptomyces avermitilis.
Batefaria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycineae, Streptomycetaceae, Streptomyces.
NGEI_TaxID=33903;
                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
SAV3762.
                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                   PRT; 186 AA.
                                   PRELIMINARY;
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                                   Q82GY4
RESULT 1
Q82GY4
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"A set of ordered oosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL939121; CABB1857.1; ...
GO; GO: Q016020; C:membrane; IEA.
GO; GO: Q0005524; F:ATP binding; IEA.
GO; GO: 00004009; F:ATP-binding cassette (ABC) transporter acti...
GO; GO: 0000166; F:nuclectide binding; IEA.
GO; GO: 0000810; P:transport; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; AAB - Lansporter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                   095039;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ABC-transporter ATP-binding protein.
SCO4666 OR SCD40A.12C OR SCD840A.12C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                   246 AA
   Mismatches
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
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ABC_transporter; 1.
AA; 1.
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STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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Nature 417:141-147(2002).
6; Conservative
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                                                                                                             12 RPPRGR 17
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ProDom; PD000006; Ā
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Cerdeno A.M.
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Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Chau C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayshizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Sukurited (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROW N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Palm C.J., Bowser L. Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.K., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Submirted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

ENBL, AY042893, AAK68833 1; -

ENBL, AY042891, AAL66880.1; -
                                                                                                                                                                                                                                                             MLN1.10.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Staryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                 Gaps
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MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
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01-NOV-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypotherical protein SCO5719.
SCO5719 OR SC3C3-105C.
SCO5719 OR ACINOBACTERIA: Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 35; DB 10; Length 255; 100.0%; Pred. No. 50;
                 Indels
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Last annotation update)
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                                                                                                                                                                  255 AA.
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100.0%; Fred. No. 48; ive 0; Mismatches
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01-DEC-2001 (TrEMBLrel. 19, Last seque
01-DEC-3003 (TrEMBLrel. 25, Last annot.
Unknown protein (Hypothetical protein)
                                                                                                                                                                 PRT;
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               6; Conservative
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                                                                             119 RPPRGR 124
Best Local Similarity
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Best Local Similarity
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                                              1 RPPRGR 6
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Q94B27;
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STRAIN=306 / ATCC 13902 / XV 101;

XX MEDLINE=202022145;
XA MEDLINE=202022145;
Ad SIGNA A.C.R., Ferror U.A., Reinach F.C., Farah C.S., Furlan L.R.,
A Quagglo R.B., Monceiro-Vitorello C.B., Van Sluys M.A., Almedda N.F.,
A Alves L.M.C., do Amaral A.M., Berrolini M.C., Camargo L.B.A.,
Camarotte G., Cannawan F., Cardozo J., Chambergo F., Clapina L.P.,
Camarotte G., Cannawan F., Cardozo J., Chambergo F., Clapina L.P.,
A Faria J.B., Ferreira A.M.S., Ferreira R.C., Ferro M.I.T.,
A Fornighieri E.F., Franco M.C., Greggio C.C., Ferro M.I.T.,
A Fornighieri E.F., Machado M.A., Madeira A.M.B.M., Martinez-Rossi N.M.,
A Martins E.C., Machado M.A., Madeira A.M.B.M., Martinez-Rossi N.M.,
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
A Spinola L.A.F., Takita M.A., Tamira R.E., Takkeira E.C., Tezza R.I.D.,
A Spinola L.A.F., Takita M.A., Tamira R.E., Takkeira E.C., Tezza R.I.D.,
A Spinola L.A.F., Takita M.A., Tamira R.E., Takkeira E.C., Tezza R.I.D.,
A Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
NCBL_TaxID=92829;
                                                                                                             Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2). Bacteria; Cyanobacteria; Chroococcales; Synechococcus. NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 35; DB 16; Length 344; Best Local Similarity 100.0%; Pred. No. 66; Matches 6; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 2; Length 332;
Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=PCC 7942;
STRAIN=PCC 7942;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U44761; AAA86647.1, -.
InterPro, IPRO0164; Crystallin.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 332 AA; 38574 MW; CA17B5F4B0F2ED09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome.
SEQUENCE 344 AA; 38396 MW; 70020FA3B0CB0B4C CRC64;
                              01.NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 100.0%; Local Similarity 100.0%; nes 6; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 RPPRGR 288
                                                                                                   ORF11692 (Fragment)
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Q8PIT0
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                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S. Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                   'Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                 100.0%; Score 35; DB 16; Length 266; 100.0%; Pred. No. 52; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 35; DB 16; Length 267; 100.0%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                            Nature 417:141-147(2002).

EMBL, AL939124; CAA20254.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 266 AA; 27842 MW; F2EFF84BF1490B3DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Biotechnol. 21:526-531(2003).

EMBL; AP005031; BAC70254.1; ...

InterPro; IPR008994; Cytok III.like.

Hypothetical protein; Complete proteome.

SEQUENCE 267 AA; 27932 MW; 7810A188389C67F8 CRC64;
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MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBZK61;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomycineae; Streptomycetaceae; Streptomyces
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Best Local Similarity 10v...
6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 RPPRGR 171
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Best Local Similarity
Matches 6; Conserv
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RESULT 5 Q82K61

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RESULT 6 Q54729 ID Q5472

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0845D0
AC 0845D0
AC 0845D
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JC
OS 00-ZA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusno J., Watanabe M., Fujimori K., Tanah H., Ishida M., Yamashita H., Chiba Y., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., Nagai K., Isogai T., Sugano S.; Subiyama A., Subinited (ocr-2001) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Protein implicated in ribosomal biogenesis, Nop56p homolog.
SIX1 OR MK0559.
Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 22, Last annotation update)
14)pochetical protein FLJ25348.
Hypochetical protein FLJ25348.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 35; DB 4; Length 378; 100:0%; Pred. No. 72; 1. ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 AA; 48515 MW; D142F8A6E8BAAA8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 378 AA; 41324 MW; D9ACAA5CACFDE88C CRC64;
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                                                                                                                                       378 AA
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STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01798; Nop; 1.
ProDom; PD004104; Nop; 1.
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Matches 6; Conservative
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                                                                                                                                       PRELIMINARY;
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Best Local Similarity
Matches 6; Conservat
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SEOUENCE 420 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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NCBI_TaxID=2320;
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Q8TXV0;
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                                                                          RESULT 8
Q96LN6
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RA MEDLINCE FROM N.A.

REQUENCE FROM N.A.

RA MEDLINE=20504483; PubMed=11016950;

RA MEDLINE=20504483; PubMed=11016950;

RA NGW W.V., Kennedy S.P., Mahairas G.S., Thorsson V., Sbrogna J.,

RA Swartzell S., Weller D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Leithauser B., Keller K., Cruz R., Krebs M.P., Angevine C.M., Dale H.,

RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

RA Isenbarcer T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

RA Elbardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Genome sequence of Halobaccerium species NRC-1.";

RGenome sequence of Lalobaccerium species NRC-1.";

"The Math. Acad. Sci. U.S.A. 97:12176-12181(2000).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-ST7-2003 (TrEMBLrel. 25, Last annotation update)
0577B11.16 protein.
0577B11.16 protein.
0772a sativa (aponica cultivar-group).
Eukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Sasaki T., Matsumoto T., Katayose Y.;
Submitva nipponbare(GA3) genomic DNA, chromosome 8, PAC clone:P0577B11.";
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005504; BAC57819.1;
InterPro; IPR002885; PPR.
PfarPANs; PF01535; PPR; 8
FIGRPANs; TGR00756; PPR; 9.
SEQUENCE 535 AA; S8557 MW; C2712C4178582982 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 35; DB 17; Length 433; 100.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                              / JCM 11081)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11 Archaea; Buryarchaecta; Halobacteria; Halobacteriaes; Halobacteriaceae; Halobacterium. NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 AA; 48104 MW; C375590B2D15DFD0 CRC64;
                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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EMBL, AE005085, AA220048.1;
PIR; D84335,
Complete protecme.
SEQUENCE 433 AA; 48104 MM
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Lag 6; Conservative
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1 RPPRGR 6
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STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann J., DeBoy R., Dedon R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE 39295987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglander K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quail M.A., Radandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Sulscon J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the blology of Mycobacterium tuberculosis from the
Complete genome sequence.";
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                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
100.0%; Score 35; DB 10; Length 535; 100.0%; Pred. No. 1e+02; ative 0; Mismatches 0; Indels 0
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Tubercuist; No. 1255; ...

GO; GO: 000564; C.nucleus; IEA.

GO; GO: 0001677; F: Draw binding; IEA.

GO; GO: 0001681; F: Xaa-Pro aminopeptidase activity; IEA.

GO; GO: 0008152; P: pretabolism; IEA.

GO; GO: 0008152; P: pretabolism; IEA.

GO; GO: 0008152; P: pretabolism; IEA.

R InterPro; IPR001005; P: pretabolism; IEA.

R InterPro; IPR001005; Myb_Dna_Dinding.

R InterPro; IPR001005; Myb_Dna_Dinding.

R Pfem; PF02129; Peptidase S15.

R Pfem; PF02129; Peptidase S15.

R TIGRPAME; TIGR00976; /NonD; 1.

R PROSITE; PS00037; MYB_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Z93777; CAB07817.1; -.
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                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Diester hydrolase, putative)
RV1215C OR MTCI364.27C OR MT1253.
Mycobacterium tuberculosis
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                                                                                                                                                                          PRT; 561 AA.
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Query Match
Best Local Similarity 100.(
Matches 6; Conservative
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                                                              1 RPPRGR 6
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STRAIN=AF2122/97;
MEDIJRE=22709107; bubMed=12788972;
MEDIJRE=22709107; bubMed=12788972;
MEDIJRE=22709107; bubMed=12788972;
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
SMOLE PROPALES SCI. W.S.A. 100:7877-7882(2003).
SRQUENCE 561 AA, 62626 MM; C35176E8172866AD CRC64;
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Bukaryota, Viridiplanica, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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NCBI_TaxID=1765;
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STRAIN-CV. Nipponbare;
STRAIN-CV. Nipponbare;
STRAIN-CV. MADENDOOR T., Yamamoto K.;
"Orryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003347; BAB86058.1; -.
EMBL; AB003452; BAB92696.1; -.
Gramene, Q8S103; -.
GO, GO:0005874; C:microtubule; IEA.
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01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
P0445E10.18 protein (P0478H03.12 protein).
                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Bust Local Similarity 100...
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536 RPPRGR 541
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Xim M.M., Bera J.G., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 3 BAC OSJNBaO079B15 genomic sequence.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Best Local Similarity 100.0%; Pred. No. 1.16+02;
Matches 6; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 35; DB 10; Length 658;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0
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Buell R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
ACO 1009043; AAPS0947.1; -.
Hypothetical protein.
SEQUENCE 658 AA; 72599 MW; AF255DB449072630 CRC64;
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007018; P:microtubule-based movement; IEA.
InterPro; IPR000217; Tubulin.
PROSITE; PS00227; TUBULIN: 1.
SEQUENCE 591 AA; 62965 MW; 6BAD242D757FD998 CRC64;
                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein OSJNBa0079B15.21.
                                                                                                                                                                                                                                                                                                                  658 AA
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                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                     213 RPPRGR 218
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112 RPPRGR 117
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Q7Y0D7;
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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPS (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are determinants of a person's susceptibility to dental caries. PRPs are fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-
                                                                                                                    Human can
Human pro
SEN virus
                                                                                                                                                                                                                                                                                                                                                                                            Human, PRP-1, proline-rich protein, saliva, dental caries,
chromosome 12p13.2, arginine catabolism, ammonia production, pH increase,
oral bacterium, caries prevention.
         Propionib
Human NOV
Human sec
Human PRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.
         Abm38646
Abr57423
Abr57423
Ada83798
Ada83798
Abg61121
Abg26281
Abg6121
Abg7681
Abg7682
Abr58878
Abr588878
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AAU32443
ABO00690
                     ABR57423
ADR856769
ADA83798
ADC98216
ABF62121
ABG26281
ABG03818
ADE07941
ABG70853
ABR58578
ADB64071
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ABP76681
AAO01213
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Result No.

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AAB48779 standard; peptide; 8 AA.
        RESULT 3
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chromosome 12p13.2; arginine catabolism, ammonia production, pH increase,
oral bacterium, caries prevention.
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                                          100.0%; Score 35; DB 4; Length 6; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
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Similarity 100.0%; Score 35; DB 4; L
Similarity 100.0%; Pred. No. 1.4e+06;
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derived oligopeptides of the invention
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6; Conservative
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Best Local Similarity
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                        Sequence 6 AA;
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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for mutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-derived oligopeptides of the invention
                                                                                                                                                 Human, PRP-1, proline-rich protein, saliva, dental caries,
chromosome 12p13.2, arginine catabolism, ammonia production, pH increase,
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chromosome 12p13.2; arginine catabolism; ammonia production; pH increase; oral bacterium; caries prevention.
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chromosome 12p13.2; arginine catabolism; ammonia production; pH increase;
oral bacterium; caries prevention.
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                                                                                                                                                                                                                                                                       (STRO/) STROEMBERG N. (JOHA/) JOHANSSON I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-031923/04
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                                                                                                       WO200069890-A1
                                                                                                                                                                                                                                                                                                                                           Stroemberg N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200069890-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                               Homo sapiens.
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                                                                                                                                                23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, PRP-1, proline-rich protein, saliva, dental caries,
chromosome 12p13.2, arginine catabolism, ammonia production; pH increase,
oral bacterium, caries prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                          New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 35; DB
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB48783 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 24; 36pp; English.
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                                                                                                            Johansson
STROEMBERG N.
JOHANSSON I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STRO/) STROEMBERG N. (JOHA/) JOHANSSON I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-031923/04.
                                                                                                                                                                               WPI; 2001-031923/04.
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                                                                                                            Stroemberg N,
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the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic

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Gaps

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100.0%; Score 35; DB 5; Length 44; 100.0%; Pred. No. 79; 0; Indels ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 6; Conservative

Sequence 44 AA;

infections

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RPPRGR 10 ø

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1 RPPRGR

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AAU53649 standard; protein; 63 AA.

RESULT 8 AAU53649

(first entry)

27-FEB-2002

AAU53649;

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The invention relates to human PRP-1-derived oligopoptides (AAB48771-ABA84878) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-derived oligopeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, nootropic, neuroprotective, cytostatic, dermatological; virucide, immunosuppressive, antihafammatory; anti-Hry; antibacterial; vulnerary; antiparkinsonian, antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiparalisegic; antidiabelic; antiuhcer; antionulsant, antignal; antiparasitic; cardiant; immune discorder; cardiovascular discrete; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 35; DB 4; Length 17; 100.0%; Pred. No. 35; o; Indels ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein SEQ ID NO 177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP62124 standard; protein; 44 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2001; 2001US-0262066P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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Brewer LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPPRGR 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP62124;
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LID. ABP1
LID. AB
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNs sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hyportrosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                       SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful fureating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bhatia A;
                                                                      Propionibacterium acnes immunogenic protein #14545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky YAW, Persing DH, Mitcham JL, Wang SS,
L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                               dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 14844; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                            21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                               20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                  Propionibacterium acnes.
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N-PSDB; AAS59562.
                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
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The invention relates to novel genes (ABQ92553-ABQ92607) and proteins (ABP62013-ABP62153) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in

Claim 11; Page 54; 785pp; English.

disorders

New polynucleotides and polypeptides useful for diagnosing, prognosing, treating or preventing e.g. neurodegenerative, central nervous system, autoimmune, respiratory, reproductive, or inflammatory diseases or

WPI; 2002-599716/64.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                 used as
and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for Pr acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
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Jones R; Carter D;
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                             100.0%; Score 35; DB 4; Length 63
100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW, Persing DH, Bhatia A, ng S, Jen S, Lodes MJ, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 14844; 1481pp; English.
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                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM50168 standard; protein; 63 AA.
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Barth B, Vallieve-Douglass J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes.
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                                                                                                                                                                                                                         Sequence 63 AA;
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patient, and a method for inhibiting the development of P. acnes in a pratient. The P. acnes polypeptides, polymuclectides, attibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polymuclectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymuclectides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the trearment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and oeteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPHO syndrome, synovitis, acne, pustulosis, hypertosis, osteomyelitis, uveitis, endophthalmitis, bone, joint, central nervous system; ELISA, inflammatory lesion, acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes immunogenic protein #1520.
                                                                                                                                                                                                                                                                                                                                    100.0%; Score 35; DB 6; I 100.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitcham JL, Wang St
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 1819; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU4,0624 standard; protein; 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001; 2001WO-US012865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Persing DH, M
o J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPPRGR 25
                                                                                                                                                                                                                                                                                                                                                                                                                RPPRGR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS59512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200181581-A2.
                                                                                                                                                                                                                                                                                               Sequence 63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2001.
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nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting ample with a binding agent that binds to the production of the invention of and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as therefore treat P. acnes infections. The antibodies may also be used as changenetic agents for determining P. acnes presence, for example, by any consyme linked immunosorbent assay (BLISA). Note: The sequence data for this patient did not form part of the printed specification, but was to wipo int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes predicted ORF-encoded polypeptide #1819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acme vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                          Length 65;
                                                                                                                                                                                                                                                                                                                        0; Indels
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Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                      / Match
Local Similarity 100.0%; Pred. No. 1.1e+02; les 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABM37143 standard; protein; 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                             1 RPPRGR 6
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                                                                                                                                                                                                                                                            Sequence 65 AA;
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                                                                                                                                                                                                                                                                                              Query Match
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Matches
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Gaps

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM64516) and to immunogenic fragments of P. acraes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared

Example 1; SEQ ID NO 1819; 1481pp; English.

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cc via this method, a vaccine composition (comprising P. acnes polypeptides, colymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient, and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnes polypeptides are useful for diagnosing, preventing or treating acnes protein. The polymucleotides can also be used as probes or primers for convolaris, or for trimulating an immune response spenies probes or primers for stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymucleotides of the remained methor. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly com WIPO at fip. wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome, synovitis, acne, pustulosis, hypertosis, osteomyelitis, uveitis, endophthalmitis, bone, joint, central nervous system; ELISA; inflammatory lesion, acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 6; Length 65; 100.0%; Pred: No. 1.1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes immunogenic protein #17581.
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Carter D;
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e J, Zhang Y, Jen S, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU56685 standard; protein; 69 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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N-PSDB; AASS9578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU56685;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), weitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acme vulgarie. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and client proteins. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (EliSA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the production, but was fire whipo.int/pub/published_pot_sequences 88888888888888888888888888

Sequence 69 AA;

; 0 100.0%; Score 35; DB 4; Length 69; 100.0%; Pred. No. 1.2e+02; 0; Indels 0; Mismatches Query Match Best Local Similarity luv... 6, Conservative 1 RPPRGR 6 g

28 RPPRGR 33

RESULT 13

ABM53204 standard; protein; 69 AA. ABM5320

ABM53204;

(first entry) 20-0CT-2003 ·

Propionibacterium acnes predicted ORF-encoded polypeptide #17880.

Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.

Propionibacterium acnes.

WO2003033515-A1.

24-APR-2003

11-OCT-2002; 2002WO-US032727.

15-OCT-2001; 2001US-00978825.

(CORI-) CORIXA CORP.

Maisonneuve JL; Jones R, Carter D; Bhatia A, Benson DR, Persing DH, Lodes MJ, Mitcham JL, Skeiky YAW, Pers: Zhang Y, Wang S, Jen S, Lod Barth B, Vallieve-Douglass J;

WPI; 2003-381789/36. N-PSDB; ACF64507.

New Propionibacterium acnes polypeptides and polymucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. Example 1; SEQ ID NO 17880; 1481pp; English

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionipacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a

polymuclectide of the invention, antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymuclecitées, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient. The P. acnes polypeptides, polymuclecitées, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the proteins. T cell populations or antigen-presenting cells that express the proteins. The polymuclecitées polymuclecitées, antibodies, fusion proteins. The polymuclecitées can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the cumulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymuclecides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly communicatives.

888888888888888888888888888888

Sequence 69 AA;

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Gaps

ô Gaps · 0 100.0%; Score 35; DB 6; Length 69; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 6; Conservative

RPPRGR 33 φ 1 RPPRGR 28

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RESULT 14 **ABM65798**

ABM65798 standard; protein; 92 AA ABM65798;

(first entry) 20-OCT-2003

Propionibacterium acnes immunogenic polypeptide #30474.

Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine; immunogenic.

Propionibacterium acnes

WO2003033515-A1.

24-APR-2003.

11-OCT-2002; 2002WO-US032727

15-OCT-2001; 2001US-00978825

(CORI-) CORIXA CORP.

ά Maisonneuve JL; Jones R, Carter Bhatia A, Benson DR, Persing DH, Lodes MJ, Mitcham JL, Skeiky YAW, Pers. Zhang Y, Wang S, Jen S, Lod Barth B, Vallieve-Douglass J;

WPI; 2003-381789/36.

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Claim 7; SEQ ID NO 30474; 1481pp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to

Claim 20; SEQ ID NO 48637; 103pp; English.

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municipantic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polymucleotide of the invention; antibodies against polypeptides of the invention; antibodies against polypeptides of the invention; antibodies against polypeptide of the invention; antibodies against polypeptide of the invention; and polypeptide of the invention; and polypeptide of the invention; and this method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polypeptides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptides of method and kit for determining the development of P. acnes in a patient. The P. acnes polypeptides, polymenting or treating acnes proteins, T cell populations or antigen-presenting cells that express the proteins, T cell populations or antigen-presenting cells that express the proteins, T cell populations or antigen-presenting cells that express the proteins, T cell populations or antigen-presenting cells that express the proteins, or for stimulating an immune response specific for a P. acnes protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present chought to contain an immunogenic region. Note The sequence data for the primer fo
polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 35; DB 6; Length 92; 100.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG18278 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US008631.
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23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping;
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Best Local Similarity 100.
Matches 6; Conservative
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N-PSDB; AAS82465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 92 AA;
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Gaps

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The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) as useful in gene therapy techniques to restore normal cutivity of (II) and to to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymuclectide sequences have applications in disposatics, forensics, gene mapping, identification of mutations in disposatics for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity and to polypeptide and polymuclecties sequences have applications in disposatic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
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Best Local Similarity 100.
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Sequence 177, App
Sequence 177, App
Sequence 223703,
Sequence 40547, A
Sequence 163482,
Sequence 51211, A
Sequence 43644, A
Sequence 174, App
Sequence 174, App
Sequence 174, App
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65233, A
63981, A
                                                                                                         April 6, 2004, 16:14:50 ; Search time 23.5514 Seconds (without alignments) 66.909 Million cell updates/sec
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Sequence 1
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/NEG_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-047-059-13703

2 US-10-424-1593-13703

2 US-10-425-114-40547

2 US-10-425-114-40547

2 US-10-425-114-51211

2 US-10-157-031-80

4 US-10-157-031-80

4 US-10-157-031-80

5 US-10-047-01-174

5 US-10-156-761-11296

2 US-10-125-114-65770

14 US-10-155-114-65730

2 US-10-425-114-65233

2 US-10-425-114-65233
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                                                                                                                                                                                                                                                                                                                          1071772 seqs, 262633353 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Sequence 57324, A Sequence 57324, A Sequence 57124, A Sequence 57494, A Sequence 74260, A Sequence 17410, Sequence 177430, Sequence 177430, Sequence 177430, Sequence 226, App Sequence 882, App Sequence 882, App Sequence 184, App Sequence 164, App Sequence 184, App	equence 53, equence 54, equence 51, equence 308, equence 85, equence 20,
US-10-425-1114- US-10-425-1114- US-10-425-1114- US-10-425-1114- US-10-425-1114- US-10-425-1114- US-10-084-896- US-10-084-896- US-10-424-599- US-10-424-599- US-10-424-599- US-10-276-174- US-10-276-174- US-10-276-174- US-10-276-174- US-10-276-174- US-10-276-174- US-10-276-174- US-10-276-174- US-10-299-105- US-10-259-165- US-10-259-165- US-10-259-165- US-10-259-165- US-10-259-165- US-10-259-165- US-10-259-165- US-10-259-165- US-10-259-165- US-10-259-165- US-10-259-165- US-10-259-165- US-10-259-165- US-09-9863-776-	US-09-863-776-5 US-09-863-776-5 US-09-863-776-5 US-09-963-776-5 US-09-946-374-3 US-09-823-187-8 US-09-863-776-2
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ALIGNMENTS

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Sequence 177, Application US/10411224

| Publication No. US20030166906A1
| Publication No. US20030166906A1
| GENERAL INPORMATION:
| APPLICANTY: Rosen et al. |
| TILLE OF INVENTION: 50 Human Secreted Proteins FILE OF INVENTION NUMBER: US/09/722, 329
| PRIOR FILING DATE: 2003-04-11
| PRIOR FILING DATE: 1999-03-04
| PRIOR APPLICATION NUMBER: 60/057, 669
| PRIOR APPLICATION NUMBER: 60/057, 669
| PRIOR FILING DATE: 1997-09-05
| PRIOR FILING DATE: 1997-09-12
| PRIOR FILING DATE: 1998-06-22
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Sequence 40547, Application US/10425114

Sequence 40547, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE PERERBUCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 40547

TENGTH: 103
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Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Can Vinua

APPLICANT: Can Vinua

APPLICANT: Cover Vongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Blants and Uses Thereof for Plant Improvement

TITLE OF SECTION WUMBER: US/10/424, 599

CURRENT APPLICATION WUMBER: US/10/424, 599

CURRENT FILING DATE: 2003-04-28

SEQ ID NO: 288684

LENGTH: 111
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100.0%; Score 35; DB 12; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 35; DB 12; Length 72; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      FEATURE:
, OTHER INFORMATION: Clone ID: PAT_MRT3847_44033C.1.pep
US-10-424-599-223703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: LIB189-001-G7_FLI.pep US-10-425-114-40547
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 223703
LENGTH: 72
                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
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ORGANISM: Glycine max
PEATURE:
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ORGANISM: Zea mays
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US-10-424-599-163482
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US-10-424-599-223703
US-10-424-599
Sequence 223703, Application US/10424599
Sequence 223703, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Apvalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
ITILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
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                                                                Gaps
Query Match
100.0%; Score 35; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION: SO Human Secreted Proteins ITILE OF INVENTION: 50 Human Secreted Proteins FILE REFERENCE: P2016P2
CURRENT APPLICATION NUMBER: US/10/047,021
CURRENT FILING DATE: 2002-01-15
FRICH APPLICATION NUMBER: US 60/262,066
PRIOR PILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 69/262,109
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/057,665
PRIOR APPLICATION NUMBER: US 60/057,665
PRIOR APPLICATION NUMBER: US 60/057,669
PRIOR APPLICATION NUMBER: US 60/057,669
PRIOR PILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/057,669
PRIOR PILING DATE: 1997-09-05
PRIOR PILING DATE: 1997-09-05
PRIOR PILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/058,974
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 60/058,974
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 60/058,974
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 60/058,974
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PRIOR APPLICATION NUMBER: US 60/058,974
PRIOR APPLICATION NUMBER: US 60/058,974
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 60/058,974
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 60/058,974
PRIOR PILING DATE: 1997-09-12
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                                                                                                                                                                                                                                                                                                                                          ; Sequence 177, Application US/10047021; Publication No. US20040002591A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-047-021-177
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US-10-047-021-177
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Sequence 80, Application US/10157031
Publication No. US20030108890A1
Publication No. US20030108890A1
Publication No. US20030108890A1
APPLICANT: Baranova, A. V.
APPLICANT: Tankovsky, N. K.
APPLICANT: Korlov, A. P.
APPLICANT: Extevoskaya, L. L.
TILLE OF INVENTION: In silico screening for phenotype-associated expressed sequences FILE REFERENCE: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: Patentin version 3.1
SEQ ID NO 80
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: EST HUYAN HIT: BROBRIES.1, EVALUE 1.00e-01
OTHER INFORMATION: SWISSPROT HIT: P02810, EVALUE 7.40e-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 35; DB 9; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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LENGIH: 132
   PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL, FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT FILING DATE: 2001-05-23
FRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-32
PRIOR FILING DATE: 2000-06-34
PRIOR FILING DATE: 2000-06-34
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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APPLICANT: Zhou, Yihua
APPLICANT: Soreen, Steven E
APPLICANT: Soreen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Danks and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 51211
LENGTH: 129
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                         CATION: (1)..(111)
COTHER INFORMATION: unsure at all Xaa locations
FEATURE:
COTHER INFORMATION: Clone ID: PAT_MRT3847_118643C.1.pep
US-10-424-599-163482
                                                                                                                                                                                                             100.0%; Score 35; DB 12; 100.0%; Pred. No. 1.6e+02;
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US-10-425-114-51211
                                                                                                                                                                                                                                                                         0; Mismatches
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Sequence 51211, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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Patent No. US20020048763A1
GENERAL INFORMATION:
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ORGANISM: Zea mays
NAME/KEY: unsure
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Matches
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Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels (
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APPLICANT: SHIRAMA, HIROSHI
APPLICANT: BAIRAM, HIROSHI
APPLICANT: BAIRAM, TADAYOSHI
APPLICANT: APARYOSHI
APPLICANT: ARAKIKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11296
LENGTH: 186
PRIOR APPLICATION NUMBER: US 09/262,109
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1998-09-03
PRIOR FILING DATE: 1998-09-03
PRIOR FILING DATE: 1998-09-03
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR PELLOGATION NUMBER: US 60/057,663
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR PILING DATE: 1997-09-12
PRIOR PLILING DATE: 1996-06-22
NUMBER OF SEQ ID NOS: 206
SOFTWARE: 1998-06-22
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; Sequence 11296, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
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US-10-156-761-11296
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 6; Conservative
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US-10-047-021-174
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LENGTH: 182
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                                                                                                                    Length 166;
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                                                                                                                                                                                0; Indels
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; Sequence 174, Application US/10047021
; Publication No. US20040002591A1
; GENERAL INFORMATION:
    TITLE REPERRICE: P2016P2
; TITLE REFERRICE: P2016P2
; CURRENT FILING DATE: 2002-01-15
; PRIOR PILING DATE: 2001-01-18
; PRIOR PILING DATE: 2001-01-18
; PRIOR FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2001-01-18
                                                                                                                 Query Match
100.0%; Score 35; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: 50 Human Secreted Proteins TITLE OF INVENTION: 50 Human Secreted Proteins CURRENT Rosen et al.

TITLE OF INVENTION: 50 Human Secreted Proteins CURRENT PELICATION NUMBER: US/10/411,224 CURRENT FILING DATE: 2003-04-11

PRIOR APPLICATION NUMBER: US/9/722,329

PRIOR FILING DATE: 1999-09-05

PRIOR FILING DATE: 1997-09-05

PRIOR FILING DATE: 1997-09-05

PRIOR FILING DATE: 1997-09-05

PRIOR PILING DATE: 1997-09-05

PRIOR PILING DATE: 1997-09-05

PRIOR PILING DATE: 1997-09-05

PRIOR PILING DATE: 1997-09-12

PRIOR PILING DATE: 1997-09-12
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Best Local Similarity 100.
Matches 6; Conservative
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CRGANISM: Homo sapiens
US-10-411-224-174
                             ; ORGANISM: Homo sapiens
US-10-157-031-80
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhoui, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Seeven E
APPLICANT: Tabaska, Jack E
APPLICANT: Plants nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBING: 38-21(53313) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 65233
LENGTH: 268
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US-10-425-114-63981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: LIB4744-011-F5_FLI.pep
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100.0%; Score 35; DB 12;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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Sequence 65770, Application US/10425114

Publication No. US200400348881

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Zbou, Yihua

APPLICANT: Avalic, David K.

APPLICANT: Tabaska, Jack E.

APPLICANT: Tabask
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US-10-425-114-65770
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US-10-156-761-10080
1S-quence 10080, Application US/10156761
1S-quence 10080, Application US/10156761
1S-quence 10080, Sprincation US/10156761
1S-quence 10080, Application US/10156761
1S-quence 10080, Application US/10156761
1S-quence 10080, Application US/10156761
1S-quence 10080, Application US/10156761
1S-quence 10080, HRCSA, HRCSHI
1S-quence 10080, HRCSA, HRCS
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Best Local Similarity 100.
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ORGANISM: Zea mays
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APPLICANT: Liu, Jingdong
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APPLICANT: Liu, Jingdong
APPLICANT: Shou, Yihua
APPLICANT: Screen, Sceven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21 [33:313] B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 63881
LENGTH: 279
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Job time: 24.5514 secs
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RESULT 14 US-10-425-114-65233 ; Sequence. 65233, Application US/10425114

167 RPPRGR 172

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Sequence 28806, A Sequence 29848, A Sequence 21411, A Sequence 19792, A Sequence 22438, A Sequence 28449, A Sequence 21480, A Sequence 21480, A Sequence 21480, A Sequence 21, Applications 4, Applications 4, Applications 28449, A Sequence 51, Applications 51, Applications 51, Applications 51, Applications 51, Applications 51, Applications 51, Applicatio
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                        April 6, 2004, 15:56:34; Search time 8.80374 Seconds (without alignments) 35.185 Million cell updates/sec
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Sequence 6
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-29848
US-09-252-991A-291451
US-09-252-991A-29505
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US-09-252-991A-17072
US-09-252-991A-28449
US-09-252-991A-28490
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S-09-252-991A-20171
S-09-252-991A-29332
S-08-403-852D-17
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-09-220-574-3
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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28 31 88.6 422 3 US-09-231-818-17 Sequence 17, Appl 29 31 88.6 422 4 US-09-635-559B-17 Sequence 17, Appl 30 31 88.6 422 4 US-09-635-559B-17 Sequence 17, Appl 31 88.6 988 4 US-08-925-48 Sequence 148, Appl 32 30 85.7 40 4 US-08-921-321-818 Sequence 16, Appl 34 30 85.7 44 US-09-635-4914 Sequence 16, Appl 35 30 85.7 50 US-08-635-4314-16 Sequence 16, Appl 36 30 85.7 72 3 US-09-635-9314-16 Sequence 16, Appl 37 30 85.7 72 3 US-09-252-991A-17022 Sequence 17022, Appl 39 30 85.7 81 4 US-09-252-991A-17022 Sequence 17022, Appl 40 30 85.7 96 4 US-09-635-247-2 Sequence 17022, Appl 41 30 85.7 98 1 US-08-150-203A-4 Sequence 4, Appl 42 30 85.7 98 1 US-08-150-203A-4 Sequence 4, Appl 42 30 85.7 98 1 US-08-150-203A-4 Sequence 4, Appl 43 30 85.7 98 1 US-08-150-203A-4 Sequence 4, Appl 44 30 85.7 98 4 US-09-252-991A-20346 Sequence 20346, Appl 46 Sequence 20345, Appl 46 Sequence 20345, Appl 56 252-991A-20346 Sequence 20346, Appl 56 252-991A-20346 Sequence 20346, Appl 56 252-991A-20346 Sequence 20346, Appl 56 252-991A-20343 Sequence 23343, Appl 56 252-991A-20343
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ALIGNMENTS

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RESULT 1
US-09-252-991A-26806

i Sequence 28806, Application US/09252991A

patent No. 6551795

i GENERAL INFORMATION:
    TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
    TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
    TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLIANG DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 175
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US-09-252-991A-29848

Sequence 28944, Application US/09252991A

Sequence 28944, Application US/09252991A

Sequence 28944, Application US/09252991A

Tathe OF INVENTION: Marc J. Rubenfield et al.

TITLE OF INVENTION: MARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

SEQ ID NOS: 33142

LENGTH: 177

TYPE: PRT
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Parent No. 6551795

Rement No. 6551795

Rement No. 6551795

GENERAL INFORMATION:

RAPPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: MACCJ. SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AGRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILLS REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILLING DATE: 1999-02-18

PRIOR FILLING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILLING DATE: 1999-07-17

REGO IN NUMBER: US 60/094,190

REGO IN NO. 17072

LENGTH: 223
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUMBER: US/08/252,991A
CURRENT APPLICATION NUMBER: US/08/252,991A
CURRENT APPLICATION NUMBER: US/08/252,991A
PRIOR PLICATION NUMBER: US 60/074,788
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR PELICATION NUMBER: 1998-02-18
PRIOR PELING DATE: 1998-07-27
NUMBER OF SEQ ID. NOS: 33142
SEGO ID NO 19798
LENGTH: 302
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53;
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100.0%; Score 35; DB
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches
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GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT / ORGANISM: Pseudomonas aeruginosa US-09-252-991A-17072
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19798
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             1 RPPRGR 6
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US-09-252-991A-22532
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21451
LENGTH: 195
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 107196.136
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1 LOCATION: (128)

7 OTHER INFORMATION: Identity of amino acid at the above locations are unknown.

US-09-252-991A-21451
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                                                                                Score 35; DB 4; Length 177; Pred. No. 43;
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                                                                                                                                     0; Indels
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PELING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                  Mismatches
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ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
                                                                          Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative 0
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Best Local Similarity
Matches 6; Conserv
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47 RPPRGR 52
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        ; OKGANISM: rseuaci
US-09-252-991A-29848
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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEUC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APPLICATION OF APPLICATION NUMBER: US/09/252,991A

CURRENT PEPRICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33.142

SEQ ID NO 24449
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILTE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 10/196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                          Length 559;
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100.0%; Score 35; DB 4; Length 746
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                0; Indels
                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28449
                                                                  ORGANISM: Pseudomonas aeruginosa US-09-252-991A-24480
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity
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               LENGIH: 559
                                         TYPE: PRT
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US 0/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR SEQIENCE 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR SEQIENCE SEQIENCE SEQIENCE SEQUENCE: 1998-07-27 NUMBER OF SEQUENCE: 1998-07-27 SEQUENCE: 13342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: APRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 418
LENGTH: 418
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APPLICANT: Marc J. Ribenfield et al.
APPLICANT: Marc J. Ribenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPRENCE: 107196, 136
CURRENT APPLICATION NUMBER: US 60/074, 788
PRICR APPLICATION NUMBER: US 60/074, 788
PRICR PILING DATE: 1998-02-18
PRICR APPLICATION NUMBER: US 60/094,190
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; Sequence 29452, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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Matches 6; Conserva
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Sequence 4, Application US/09123624

| Patent No. 6149936
| APPLICANT: SCHRADER, Jurgen
| APPLICANT: GCHRADER, JACA
| TILLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
| TILLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
| TILLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
| TILLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
| TILLE OF INVENTION: 08/09/123, 624
| CURRENT APPLICATION NUMBER: 08/553,503
| PRIOR FILING DATE: 1994-03-01
| PRIOR FILING DATE: 1994-03-31
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09123708

| Sequence 4, Application US/09123708
| Patent NO. 6146887
| GENERAL INFORMATION:
| APPLICANT: SCHRADER, Juergen
| APPLICANT: GOSDECKE, Axel
| TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
| TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
| TITLE OF INVENTION: DATE: 1990-07-28
| FILE REPRENCE: 511169-2033
| CURRENT FILING DATE: 1996-03-01
| EARLIER FILING DATE: 1996-03-01
| EARLIER APPLICATION NUMBER: P4411402.8
| EARLIER APPLICATION NUMBER: P4411402.8
| SERIER PILING DATE: 1994-03-31
| SOFTWARE: PATENTING DATE: 1994-03-31
| SOFTWARE: PATENTING DATE: 1994-03-31
| SOFTWARE: PATENTING DATE: 1994-03-31
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Pred. No. 9.1e+02;
1; Mismatches 0;
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91.4%; Score 32; DB
Best Local Similarity 83.3%; Pred. No. 9.1e
Matches 5; Conservative 1; Mismatches
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83.3%;
         LENGTH: 1433 amino acids
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Best Local Similarity 83.3
Matches 5; Conservative
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TYPE: PRT
CORGANISM: Cytomegalovirus
US-09-123-708-4
                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-365-486A-21
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ORGANISM: Homo sapiens
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US-09-123-624-4
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US-09-252-991A-28997
Sequence 28997, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
PAPLICANTON: NATCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28997
LENGTH: 295
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| Patent No. 584306
| GENERAL INFORMATION:
| APPLICANT: Webster, Keith A. APPLICANT: Webster, Namette H. TITLE OF INVENTION: Therapeutic Constructs
| TITLE OF INVENTION: Therapeutic Constructs
| NUMBER OF SEQUENCES: ADDRESSE: ADDRESSE: Deblinger & Associates
| STREE 350 Cambridge Avenue, Suite 250 CITY: Palo Alto
| STATE: CA COUNTRY: USA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 295;
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Pred. No. 2.2e+02;
1; Mismatches 0; Indels
    Indels
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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K,
REGISTRATION NUMBER: 36,615
REFERENCE/DOCKET NUMBER: 85,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION 1924-0880
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  0; Mismatches
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28997
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.37
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6; Conservative
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                                            1 RPPRGR 6
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US-08-365-486A-21
Matches
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Best Local Similarity 83.3%; Pred. No. 9.18+02; Matches 5; Conservative 1; Mismatches 0; Indels

1 RPPRGR 6 :||||| 515 KPPRGR 520

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Search completed: April 6, 2004, 16:19:41 Job time : 8.80374 secs

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Q8r5m2 Q22289 P03230

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12.10TL-1986 (Rel. 01, Created)
01.MAR-1989 (Rel. 10, Last sequence update)
15.MAR-2004 (Rel. 43, Last annotation update)
15.MAR-2004 (Rel. 43, Last annotation update)
15.MAR-2004 (Rel. 43, Last parction update)
16.MAR-2004 (Rel. 43, Last phosphoprotein 1/2 precursor (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (Protein A/protein C) (Contains: Peptl AND PRH2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE OF 17-166 (PRP-2).
MEDLINE=6622216; PubMed=3710693;
Schlesinger D.H., Hay D.I.;
"Complete covalent structure of a proline-rich phosphoprotein, PRP-2, an inhibitor of calcium phosphate crystal growth from human parotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ALLELES PRH2-1 AND PRH1-PIF).
MEDLINE=85289325; PubMed=2993301;
Maeda N., Kim H.-S., Azen E.A., Smithies O.;
"Differential RNA splicing and post-translational cleavages in the human salivary proline-rich protein gene system.";
J. Biol. Chem. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 17-166 (PRP-1 TO PRP-4; PIF-F AND PIF-S).
MEDLINE=89061650; PubMed=3196309;
Hay D.I., Bennick A., Schlesinger D.H., Minaguchi K.,
Madapallimattam G., Schluckebier S.K.;
"The primary structures of six human salivary acidic proline-rich protein (PRP-1, PRP-2, PRP-3, PRP-4, PIF-s and PIF-f).";
Biochem. J. 255:15-21(1988).
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 17-166 FROM N.A. (PA ALLELE).
MEDLINE=88074309; PubMed=3687941;
Azen E.A., Kim H.S., Goodman P., Flynn S., Maeda N.;
"Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich proteins Pa, Db, and PIF.";
Am. J. Hum. Genet. 41:1035-1047(1987).
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CTD5_HUMAN
                                         CAEEL
                                                                                    MOUSE
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HTL1C
                                                                   EBVR
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MEDLINE=80204368; PubMed=7380845;
Wong R.S.C., Bennick A.;
                                                      LMP1
LMP1
BM15
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GAG H
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 RESULT 1
PRPC_HUMAN
ID PRPC_HUMAN
AC P028I0;
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                                                                                                    6, 2004, 15:31:19; Search time 3.86916 Seconds (without alignments) 80.746 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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TRPD_HALVO
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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BIND

PEPTIDE P-C. INHIBIT HYDROXYAPATITE FORMATION,

166 46

122

PHOSPHOPROTEIN 3/4.

SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2. SALIVARY ACIDIC PROLINE-RICH

TO HYDROXYAPATITE AND CALCIUM. PYRROLIDONE CARBOXYLIC ACID.

PHOSPHORYLATION PHOSPHORYLATION

122 238 20 20

D -> N (in allele PRH1-4).

/FTIG=VAR 005563.
D -> N (in allele PRH2-1).
/FTIG=VAR 005564.
/FTIG=VAR 005567.
F -> P (IN REF 10).

N

us-10-009-709-11.rsp

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MIM; 168730; -.
MIM; 168790; -.
MIM; 168710; -
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Genew; HGNC:9367; PRH2.
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Local Similarity 100
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P52562;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Azen E.A.;
"A frequent mutation in the acidic proline-rich protein gene, PRH2,
causing a Q147K change closely adjacent to the bacterial binding
domain of the cognate salivary PRP (Prl') in Afro-Americans.";
Hum. Mutat. 12:72-72(1998).
-!- FUNCTION: PRP's act as highly potent inhibitors of crystal growth
-!- FUNCTION: PRP's act as highly potent inhibitors and reparative
of calcium phosphates. They provide a protective and reparative
environment for dental enamel which is important for the integrity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlesinger D.H., Hay D.I.; "Complete primary structure of a proline-rich phosphoprotein (PRP-4), a potent inhibitor of calcium phosphate precipitation in human parotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted.

PTM: Proteolytically cleaved; PRP-2, PRP-1, and PIF-S yield PRP-4, PRP-3 (protein A), and PIF-F, respectively.

POLYMORPHISM: Allele PRH1-4 is also known as PRH1 DA allele; allele PRH2-1 is also known as PRI or protein C; allele PRH2-3 is also known as PRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE OF 123-166 (PEPTIDE P-C).
MEDLINE-80227634; PubMed-7390979;
ISemura S., Saltoh E., Sanada K.;
"The amino acid sequence of a salivary proline-rich peptide, P-C, and the relation to a salivary proline-rich phosphoprotein, protein C.";
J. Biochem. 87:1071-1077 (1980).
                                                                                                                                                                                                                                                                                                                                                                                 proline-rich phosphoprotein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (In) Gross E., Meienhofer J. (eds.);
septides: structure and biological function (Proceedings of the 6th
American peptide symposium), pp.133-136, Pierce Chemical Co.,
Rockford II. (1979).
"The primary structure of a salivary calcium-binding proline-rich
phosphoprotein (protein C), a possible precursor of a related
                                                                                                                                                                                                      human and
                                                                                                                             SEQUENCE OF 17-46 (PROTEIN C).
MEDLINE-81191179; PubMed=7228490;
Schlesinger D.H., Hay D.I.;
Primary structure of the active tryptic fragments of
monkey salivary anionic proline-rich proteins.";
Int. J. Pept. Protein Res. 17:34-41(1981).
                                                                                                                                                                                                                                                                                                                                 MEDLINE=79173237; PubMed=438215; WONG R.S.C., Hofmann T., Bennick A.; Hithe complete primary structure of a human saliva.";
                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 254:4800-4808(1979).
                                                          salivary protein A.";
J. Biol. Chem. 255:5943-5948(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 17-122 (PROTEIN A).
                                                                                                                                                                                                                                                                                                            SEQUENCE OF 17-122 (PROTEIN A)
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EMBL; K03203; AAA60184.1; --
EMBL; M13057; AAA98807.1; --
EMBL; M13058; AAA98808.1; --
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Gaps

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0; Indels

0; Mismatches

100.0%; Score 35; DB 1; Length 166; 100.0%; Pred. No. 7.8;

-> P (IN REF. 10). A7DF62BF94E3C3EF CRC64;

17017 MW;

163

99

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                                                                                                                                                                                                                  ProDom, PD001864; Glyco_trans_3; 1.
TIGREAMS; TIGR01245; trpD; 1.
Tryptophan biosynthesis; Transferase; Glycosyltransferase.
                                                                                              Halobacterium volcanii (Haloferax volcanii).
Archaea, Euryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Haloferax.
                                    01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Anthranilate phosphoribosyltransferase (RC 2.4.2.18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, M83788; AAA73175.1; -.
HAMAP; MT_00211; -; 1.
InterPro; IPR00594; dlyco_trans.
InterPro; IPR000312; dlyco_trans_3.
Pfam; PP02885; Glycos_trans_3.
Pfam; PF00591; Glycos_trans_31; 1.
                                                                                                                                                                                              STRAIN=WFD11;
MEDLINE=92165748; PubMed=1537810;
                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq.
10-0CT-2003 (Rel. 42, Last anno
STANDARD;
                                                                                                                                                                                SEQUENCE FROM N.A.
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Bukaryota, Metazoa Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Dullio A., Faraonio R., Minopoli G., Zambrano N., Russo T.;
Prefsiz: a new member of the Pe65 protein family interacting with the "Fe6512: a new member of the Pe65 protein family interacting with the intracellular domain of the Alzheimer's beta-amyloid precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.";
Biochem. J. 330:513-519(1998).

-!- FUNCTION: MAY MODULATE THE INTERNALIZATION OF BETA-AMYLOID
PRECURSOR PROTEIN.

-!- SUBUNIT: BINDS TO THE INTRACELLULAR DOMAIN OF THE BETA-AMYLOID
PRECURSOR PROTEIN. ALSO BIND TO APP-LIKE PROTEINS.

-!- TISSUE SPECIFICITY: EXPESSED PREDOMINANTLY IN BRAIN AND TESTIS.

-!- SIMILARITY: CONTAINS 1 WM domains.

-!- SIMILARITY: CONTAINS 2 PID domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID 1.
PID 2.
Missing (in isoform I).
/FIId=VSP 006799.
D -> PISAPA (in isoform III).
/FIId=VSP 006800.
D -> DSPISAPA (in isoform IV).
/FIId=VSP 006801.
/FIId=VSP 006801.
/FIId=VSP 006801.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Amvloid beta A4 precursor protein-binding family B protein 2).
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Pred. No. 83;
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S; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MAO Y.M., Yie Y., Sun Z., Chen X.M., Ying K., Dai J.L., Lin S., Mu C.Q., Li Y., Whu C.Q., Li Y., "Molecular cloning of the full-length cDNA and novel splicing isoforms
                                                                                                                                                                                                                                                                                                                                                                                                       095704; 09NYX6; 09NYX7; Q9NYX8; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 45 precursor protein-binding family B member 3 (Pe65-like protein 2).
                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: BINDS TO THE INTRACELLULAR DOMAIN OF THE BETA-AMYLOID PRECIRESOR PROTEIN. ALSO BIND TO APP-LIKE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome structure and chromosomal mapping of the gene for Fe65L2 interacting with Alzheimer's beta-amyloid precursor protein."; Biochem, Biophys. Res. Commun. 258:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tanahashi H.;
"Molecular cloning of human Fe65L2 and its interaction with the Alzheimer's beta-amyloid precursor protein.";
Neurosci. Lett. 261:143-146(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Fe65L2 gene.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY MODULATE THE INTERNALIZATION OF BETA-AMYLOID
PRECURSOR PROTEIN.
                                                          100.0%; Score 35; DB 1; Length 337; 100.0%; Pred. No. 16; 0; Mismatches 0; Indels
   337 AA; 34551 MW; 13ECFAF2A0AE941E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=095704-4; Sequence=VSP_006801;
--- TISSUB SPECIFICITY: EXPERSEND IN VARIOUS TISSUBS.
---- SIMILARITY: Contains 1 WW domain.
---- SIMILARITY: Contains 2 PID domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=095704-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=095704-3; Sequence=VSP_006800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS I AND II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99262108; PubMed=10329396; 
Tanahashi H., Tabira T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99180006; PubMed=10081969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM II)
                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                            Similarity
                                                                                                                                                                                                                                    RPPRGR 26
                                                                                                                                                                               RPPRGR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APBB3 OR FE65L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                        ABB3 HUMAN
                                                          Query Match
Best Local S
            SEQUENCE
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Gaps

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Gaps

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Indels

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Mismatches

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5; Conservative
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51 KPPRGR 56
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                                1 RPPRGR
                                                                                                                                          Z384 HUMAN
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                                                                                                                    Z384_HUMAN
   Matches
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use by non-profit institutions of removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
MEDILINE-97305956, PubMed-9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A., Perset X.,
"Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
-- SIMILARITY: VERY LOW SIMILARITY TO THE IS21/IS408/IS1162 FAMILY OF
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid sym_pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                          Similarity 83.3%; Pred. No. 86; 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 504;
                                                                                                                                                                                                                                              29 61 WW.
117 252 PID 1.
288 413 PID 2.
504 AA; 54907 MW; A49CA9E99BDB3A3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ll protein; Plasmid.
504 AA; 57228 MW; 63E31E487DD4CB87 CRC64;
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86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Hypothetical 57.2 kDa protein Y4JA/Y4NE/Y4SE.
Y4JA AND Y4NE AND Y4SE.
Rhizobium sp. (Strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32;
Pred. No.
                                                                                     InterPro; IPR006620; PTB PIC.
InterPro; IPR006620; PTB PIC.
InterPro; IPR001202; WW Rep5_WWP.
Pfam; PP000540; PID; 2.
SWART; SM00462; PTB; 2.
SWART; SM00462; PTB; 2.
PROSITE; PS01179; PID; 2.
PROSITE; PS01179; WW DOMAIN 1; 1.
PROSITE; PS00120; WW DOMAIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: STRONG, TO FZ4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE0000079; AAB91713.1; -. EMBL; AE000086; AAB91785.1; -. EMBL; AE000095; AAB91845.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.4%;
83.3%;
                                                                          EMBL; Y13413; CAA73837.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001584; Rve.
Pfam; PF00665; rve; 1.
Hypothetical protein; Pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   78 RPPKGR 83
                                                                                                                                                                                                                                                                                                                                                                                        1 RPPRGR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y4JA RHISN
P55501;
                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                   Repeat.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                          Tanigami A.I.; Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamateu A., Ishii S., Yanamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yanashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nadai K., Isogai T., Sugano S., Nagahari K., Subanited (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Transcription factor that binds the consensus DNA sequence [GC]AAAAA. Seems to bind and regulate the promoters of MMP1, MMP3, MMP7 and COLIA1 (By similarity).
-!- SUBUNIT: Interacts with Cas (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain cortex;
MBDLINE=97369492; PubMed=9225980;
Margolis R.L., Abraham M.R., Gatchell S.B., Li S.-H., Kidwai A.S.,
Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;
"CDNAs with long CAG trinucleotide repeats from human brain.";
Hum. Genet. 100:114-122(1997)
                                                                                                                                                                         Sukaryoča, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isold=08TF68-2; Sequence=VSP 006920;
ILLARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
QBTFE8, O15407; QBN938; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-CCT-2003 (Rel. 42, Last sanotation update) 2inc finger protein 384 (Nuclear matrix transcription factor 4) (CAG repeat protein 1). 2NF384 OR NM4 OR CAGH1.
                                                                                                                                                                                                                                                                               Matsuo M.Y.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 8 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q8TF68-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB070238; BAB85125.1; -.
EMBL; AK095734; BAC04618.1; -.
EMBL; U80738; AAB91437.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 395-576 FROM N.A.
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Isoid=09EQJ4-3; Sequence=VSP 006922;
TISSUE SPECIFICITY: Expressed in osteocytes, osteoblasts, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.4%; Score 32; DB 1; Length 579; 83.3%; Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTIG=VSF_006921.
Missing (In isoform 3).
FTIG=VSF_006922.
GG -> RS (IN REF. 1).
LA -> WP (IN REF. 1).
                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 8 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   614 AA.
                                                                                   IsoId=Q9EQJ4-2; Sequence=VSP_006921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                    IsoId=Q9EQJ4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AB019281; BAA89664.1; -.. EMBL; AF216804; AAG40582.1; -. EMBL; AF216805; AAG40583.1; -. EMBL; AF216806; AAG40584.1; -. HSSP; PO8153; 1ZFD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63139 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                                                                                                                                                                                                   FINGER PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFAC; TO5136; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 KPPRGR 195
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Q10600;
                                                                                                             Name=3;
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                                                                                | NEW 
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MEDLINE-20136045; PubMed=10669742;
Makamoto T., Yamagata T., Sakai R., Ogawa S., Honda H., Ueno H., Hirano N., Yazaki Y., Hirai H.;
"CIZ, a zinc finger protein that interacts with pl30cas and activates the expression of matrix metalloproteinases.";
Mol. Cell. Biol. 20:1649-1658(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bone Miner. Res. 16.10-23(2001).
-!- FUNCTION: Transcription factor that binds the consensus DNA
sequence [GC]AAAAA. Seems to bind and regulate the promoters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thunyakitpisal P., Alvarez M., Tokunaga K., Onyia J.E., Hock J., Ohashi N., Feister H., Rhodes S.J., Bidwell J.P.; "Cloning and functional analysis of a family of nuclear matrix transcription factors (NP/NMP4) that regulate type I collagen expression in osteoblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2384_RAT STANDARD, PRT; 579 AA.
OPEQU4; OPEQU3; Q9MJ5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 384 (Nuclear matrix transcription factor 4)
(Cas-associated zinc finger protein).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2A152786C3C46D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform 2). /FTId=VSP 006920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MMP1, MMP3, MMP7 and COLLA1.
SUBGUNIT: Interacts with Cas.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                          GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21024193; PubMed=11149472;
                       InterPro; IPR007087; Znf C2H2.
Pfam; PF00096; zf-C2H2; B.
ProDom; PD000003; Znf_C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63091 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative 7
  Genew; HGNC:11955; ZNF384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 AA;
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189 KPPRGR 194
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                                                                                                                                                                                                                                                                                                                                                                                                                    461
466
300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Z384 RAT
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TRANSFAC; TRANSFAC; TO51...

TRANSFAC; TO5141; -..

R TRANSFAC; TO5142; -..

DR TRANSFAC; TO5142; -..

DR Probom; PR001089; ZHC CZH2; B.

DR PROSITE; PS001081; ZIMC CZH2; B.

DR PROSITE; PS001081; ZIMC FINGER CZH2; B.

RW Transcription regulation; ZiMC FINGER CZH2; B.

KW Transcription regulation; ZiMC FINGER CZH2; B.

KW Transcription regulation; ZiMC FINGER CZH2-TYPE 1.

RM DNA-binding; Repeat; Alternative splicing.

PT ZN FING 229 251 CZH2-TYPE 2.

FT ZN FING 285 307 CZH2-TYPE 3.

FT ZN FING 318 340 CZH2-TYPE 5.

FT ZN FING 346 CZH2-TYPE 6.

FT ZN FING 404 426 CZH2-TYPE 7.

AMSSING (in isoform 2).

AMSSING (in isoform 2).

AMSSING (in isoform 3).

AMSSING (in isoform 3).
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CysN/cysC bifunctional enzyme [Includes: Sulfate adenylyltransferase
chondrocytes in bone.
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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laboratory strains."
                             SEQUENCE FROM N.A.
           SEQUENCE FROM N.A.
                                                                                FIGE; MT1324; -
        NCBI_TaxID=1773;
                                                               family
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MEDLINE_20090929; PubMed=10623522; Zhang M.; Tochio H., Hung F., Li M., Bredt D.S., Zhang M.; Solution structure and backbone dynamics of the second PDZ domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-95212184; PubMede8626668;
Silvagno F., Xia H., Bredt D.S.;
Silvagno F., Xia H., Bredt D.S.;
"Neutronal nitric-oxide synthase-mu, an alternatively spliced isoform
expressed in differentiated skeletal muscle.";
J. Biol. Chem. 271:11204-11208(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS N-NOS-1 AND N-NOS-2).
STRAIN=BALB/c; TISSUE=Brain;
MEDILFRE=9312288; PubMed=7686743;
MEDILFRE=9312288; PubMed=7686743;
MEDILFRE=9312288; PubMed=7686743;
MEDILFRE=9312288; PubMed=70115888 H., Kurashima Y., Esumi H.;
"Structural diversity of neuronal oxide synthase mRNA in the nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NAY-2000 (Rel. 39, Created)
30-NAY-2000 (Rel. 39, Last sequence update)
15-NAR-2004 (Rel. 43, Last annotation update)
115-NAR-2004 (Rel. 43, Last annotation update)
115-NAR-2006 (Rel. 39, Creatitutive NoS) (NC-NOS) (BNOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE SPLICING (ISOFORMS NNOS BETA; NNOS GAMMA AND NNOS MU).
MEDLINE=97351924; PubMed=9208206;
Brenman J.E., Xia H., Chao D.S., Black S.M., Bredt D.S.;
"Regulation of neuronal nitric oxide synthase through alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
InterPro; IPR009000; Translat_factor.

Pfam; PF00109; GTP_EFTU; 1.

PFam; PF00109; GTP_EFTU; 1.

R Pfam; PF00109; GTP_EFTU; 1.

R PF03144; GTP_EFTU; 1.

R PF03144; GTP_EFTU; 1.

R PRODM; PD002350; ABS_Kinase; 1.

R TIGREAMS; TIGROGAS; apsK; 1.

R ROSITE; PS00301; EFACTOR_GTP; 1.

R Cystaine biosyntheeis; Transferase; Nucleotidyltransferase; Cystaine biosynthesis; Transferase; M GTP-binding; Minase; ATP-binding; Multifunctional enzyme; Complete proteome.

M Omplete proteome.

T DOMAIN 1 44 ADENYLYLSULEATE KIRASE.

T DOMAIN 11 64 ADENYLYLSULEATE KIRASE.

T NP_BIND 11 18 GTP (BY SIMILARITY).

T NP_BIND 450 457 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                          SULFATE ADENVLYL TRANSFERASE.
ADENVLYLSULFATE KINASE.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
ATP (POTENTIAL).
PHOSPHOSERINE INTERMEDIATE
                                                                                                                                                                                                                        Nucleotidyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.4%; Score 32; DB 1; Length bla
83.3%; Pred. No. 1.1e+02;
83.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
2C3709C8B91867C4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM NNOS MU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614 AA; 67838 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        postsynaptic density-95.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                              614
18
92
146
457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 RPPRGK 444
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les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RPPRGR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _NOS1_MOUSE ST
Q9Z0J4; Q64208;
30-MAY-2000 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ". Bacteriol. 184:5479-5490(2002).

-!- FUNCTION: ATP Sulfurylase may be the GTPase, regulating ATP sulfurylase activity (By similarity).

-!- FUNCTION: APS kinase catalyzes the synthesis of activated sulfate.

-!- FUNCTION: APS kinase catalyzes the synthesis of activated sulfate.

-!- FUNCTION: APS KINASE AT + sulfate = diphosphate + adenylylsulfate.

-!- CALLYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subunit 1 (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase large subunit); Adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (ATP adenosine-5'-phosphosulfate 3'-phosphotransferase)).
CYSNC OR CYSN OR RV1286 OR WT1324 OR MTCY373.05.
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                                                                                                                                                                                                                                                                                                                                                                                                                s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CDC 1551 / Oshkosh,
MEDLINE=2220649; PubMed=12218036;
Rleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphoadenylylsulfate.
--- PATHWAY: Sulfate activation; cysteine biosynthesis reductive branch; first step.
--- PATHWAY: Sulfate activation; cysteine biosynthesis reductive branch; second step.
--- SUBUNIT: Heterodimer composed of cysD, the smaller subunit, and
                                                                                                                                                                                                                                                                                                                                         Harris
                                                                                                                                                                                                                                                                                                MEDLINE=9829597, PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekala F., Davies R., Badcock K., Basham D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculist; Rv1286; -.
HAMAP; MF_00062; fused; 1.
HAMAP: MF_00065; fused; 1.
InterPro; IPR002891; APS_kinase.
InterPro; IPR0020795; EF_GTPbind.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR009001; Elong_init_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z73419; CAA97752.1; -. EMBL; AE007007; AAK45585.1; PIR; B70772; B70772. HSSP; P02990; 1ETU.
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Gaps

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Length 614;

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1. Mol. Biol. 295:225-237(2000).

1. FUNCTION: Produces nitric oxide (NO) which is a messenger molecule with diverse functions throughout the body. In the brain and peripheral nervous system, NO displays many properties of a neurotransmitter. Isoform NNOS Mu may be an effector enzyme for the dystrophin complex.

1. CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+)

1. COPACTOR: Heme. Binds one mole each of FAD and FAN. Also requires tetrahydrobiopterin (BH4) which may stabilize the dimeric form of the enzyme (By similarity).

1. ENZYME REGULATION: Stimulated by calcium/calmodulin. Inhibited by n-Nos-inhibiting protein (BHN) which may prevent the dimerization of the protein (By similarity).

2. SUBCELLULAR LOCATION: Interacts with DiG4.

3. SUBCELLULAR LOCATION: In skeletal muscle, it is localized beneath dystrophin glycoprotein complex.

4. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDUCTION: By Choice and Sequence of the neurous system:

Sequence Nos Win Synonyms-Muscle-specific;

Isold=Q9Z074-4; Sequence=VSP_00357;

Name=NNOS Win; Synonyms-Muscle-specific;

Isold=Q9Z074-4; Sequence=VSP_00357;

Isold=Q9Z074-5; Sequence=VSP_00357;

Sequence=VSP_00357;

TISSUE SPECIFICITY: Widely expressed in the nervous system:
expressed in cerebrum, olfactory bulb, hippocampus, midbrain,
cerebellum, pons, medulla oblongata, and spinal cord. Also found
in skeletal muscle, where it is localized beneath the sarcolemm
of fast twitch muscle, where it is localized beneath the sarcolemm
of fast twitch muscle, where it is localized beneath the sarcolemm
of fast twitch muscle, where it is localized beneath the sarcolemm
of fast twitch muscle, where it is localized beneath the sarcolemm
of fast twitch muscle, where it is localized beneath the sarcolemm
of fast twitch muscle fibers, and in all parts of the nervous
the brain and NNOS beta expression is developmentally regulated.

NNOS Mu is only found in mature skeletal and cardiac muscles.

INDUCTION: By cholinergic agonists acting at inositel phosphate-
liked muscastinic receptors in cardiac mycoytes.

INDUCTION: By cholinergic agonists acting at inositel phosphate-
liked muscastinic receptors in cardiac mycoytes.

ISONOR Mu is only found in mit the N-terminal part of the neuronal isoform participates in protein-protein interaction, and is responsible for targeting nNos to synaptic membranes in muscles.

JOMAIN: The PDZ domain in the N-terminal part of the neuronal stream and accumulates in the cytosol.

SIMILARITY: Contains I flavodoxin-like domain.

SIMILARITY: Contains I flavodoxin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isold=Q9Z0J4-3; Sequence=VSP_003575, VSP_003576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:97360; Nosl.
GO:0045202; C:synaptic junction; IDA.
GO:0045202; C:synaptic junction; IDA.
InterPro; IPR001094; Flav nitox synth.
InterPro; IPR001094; Flavdoxin like.
InterPro; IPR001094; Flavdoxin like.
InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR004030; No Synthase.
InterPro; IPR004030; No Synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=N-NOS-2;
IsoId=Q9Z0J4-2; Sequence=VSP_003578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=N-NOS-1;
IsoId=Q9Z0J4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D14552; BAA03415.1; -.
EMBL; S81982; AAB36469.1; -.
PIR; JN0609; JN0609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001433; Oxre
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=NNOS beta;
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(BY SIMILARITY).
FLAVODOXIN-LIKE.
IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_003575.
TGIQVD -> MRGLGS (in isoform NNOS beta).
/FTId=VSP_003576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K -> KYPEPLRFFPRKGPSLSHVDSEAHSLVAARDSQHR (in isoform NNOS Mu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=95105197; PubMed=7528745;
Hall A.V., Antoniou H., Wang Y., Cheung A.H., Arbus A.M., Olson S.L.,
Lu W.C., Kau C.-L., Marsden P.A.;
"Structural organization of the human neuronal nitric oxide synthase
gene (NOS1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      CALMODULIN-BINDING (POTENTIAL).
PRIN (PYRIMIDINE PART) (BY SIMILARITY).
PAD (ADP PART) (BY SIMILARITY).
PAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
MADP (ADP PART) (BY SIMILARITY).
Missing (in isoform NNOS beca).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Nitric-Oxide synthase, brain (EC 1.14.13.39) (NOS, type I) (Neuronal NOS) (N-NOS) (NNOS) (Constitutive NOS) (NC-NOS) (bNOS).
                                                                                                                                                                                                                                                                                                                             NNOS-INHIBITING PROTEIN (PIN) - BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IISSUE=Cerebellum;
MBDLINE=94267447; PubMed=7515942;
Fujisawa H., Ogura T., Kurashima Y., Yokoyama T., Yamashita J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (In isoform NNOS gamma).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FIId=VSP 003577.
Missing (in isoform N-NOS-2).
                                                                                                                                                                                                                                          Oxidoreductase, NADP, FAD, FWN, Calmodulin-binding, Heme, Alternative splicing, Multigene family.

DOMAIN
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                                                                                                                                                                                 PROSITE; PSS0902; FLAVODOXIN_LIKE; 1.
PROSITE; PS60001; NOS; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 269:33082-33090(1994).
FAD binding 1; 1. flavodoxin; 1.
                        Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD binding 1; 1.
Pfam; PF02898; NO Synthase; 1.
Pfam; PP00595; PDZ; 1.
                                                                                                            PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
SMART; SM00228; PDZ; 1.
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Matches 5; Conservative
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P29475;
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NOS1 HUMAN
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Event-Alternative splicing; Named isoforms=4;

Comment=Isoform 3 is produced by different alternative splicing events implicating either the untranslated exons TERI (TNNOS) overtes implicating either the untranslated exons TERI (TNNOS) or TEXIB (TNNOS) leading to a N-terminus truncated protein which possesses enzymatic activity comparable to that of isoform 1. The C-terminal truncated isoform 4 is produced by insertion of the TEX2 exon between exons 3 and 4 of isoform 1, leading to a frameshift and a premeture stop codon;

Name=1. Synonyma=N-NOS-1;

Name=2; Synonyma=N-NOS-1;

Name=2; Synonyma=TEX2-insertion;

Isoid=P29475-2; Sequence=VSP 003574;

Name=3; Synonyms=TEX2-insertion;

Isoid=P29475-3; Sequence=VSP 003572;

Name=4; Synonyms=TEX2-insertion;

Isoid=P29475-4; Sequence=VSP 003572;

Name=4; Synonyms=TEX2-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang Y., Goligorsky M.S., Lin M., Wilcox J.N., Marsden P.A.;
"A novel, testis-specific mRNA transcript encoding an NH2-terminal
truncated nitric-oxide synthase.";
J. Biol. Chem. 272:11392-11401(1997).
-!- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule
with diverse functions throughout the body. In the brain and
paripheral nervous system, NO displays many properties of a
neurotransmitter.
-!- CATALYTIC ACTUVITY: L-arginine + N NADPH + M O(2) = citrulline +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBDIVITY FORGINGER. Interacts with DLG4 (By similarity). Forms a ternary complex with CAPON and RASD1.
SUBCELLUIAR LOCATION: In skeletal muscle, it is localized beneath the sarcolemma of fast-twitch muscle fiber by associating with the
                                                                                                                                                       TISSUE=Brain;
MEDLINE=9313039; PubMed=7678401;
Nakane M., Schmidt H.H.H.W., Pollock J.S., Foerstermann U., Murad F.;
Nakane M., Schmidt H.H.H.W., Pollock J.S., Foerstermann U., Murad F.;
NCloned human brain nitric oxide synthase is highly expressed in skeletal muscle.";
FEBS Lett. 316:175-180(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                               Park C.-S., Gianotti C., Park R., Krishna G.;
"Neuronal isoform of nitric oxide synthase is expressed at low levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitric oxide + N NADP(+).
-!- COFACTOR: Heme, Binds one mole each of FAD and FMN. Also requires tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENZYME REGULATION: Stimulated by calcium/calmodulin. Inhibited by n-Nos-inhibiting protein (PIN) which may prevent the dimerization of the protein.
                    "Expression of two types of nitric oxide synthase mRNA in human neuroblastoma cell lines.";
J. Neurochem. 63:140-145(1994).
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SIMILARITY: Belongs to the NOS family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell. Mol. Neurobiol. 16:499-515(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
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                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Retina;
MEDLINE=97034095; PubMed=8879752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Testis;
MEDLINE=97269048; PubMed=9111048;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human retina.";
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CC -1- SNULARIY: Contains 1 PRAVOGATIL | If anomain.
-1- SNULARIY: Contains 1 PRAVOGATIL | If anomain.
-1- SNULARIY: Contains 1 PRAVOGATIL | If a produced through a collaboration contains 1 PRAVISE and the statement of the statement of the statement of the statement of the statement is not removed. Usage by and for commercial continues as included and the statement is not removed. Usage by and for commercial continues as included and for commercial continues as included and for statement is not removed. Usage by and for commercial continues as included and for statement is not removed. Usage by and for commercial continues as included and for statement is not removed. Usage by and for commercial continues as included and for statement is not removed. Usage by and for commercial continues as included and for statement is not removed. Usage by and for commercial continues as included and for statement is not removed. Usage by and for commercial continues as included and for statement is not removed. Usage by and for commercial continues as included and for statement is not removed. Usage by and for commercial continues as included and for commercial continues as included and for statement is not removed. Usage by and for commercial continues as included and for commercial continues as included and for commercial continues as included and for continues and for continues as included and for continues and for contin
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WER (in isoform 4).

### / FIL = VSP 003572.

### / FIL = VSP 003573.

### / FIL = VSP 003574.

### / V -> L (IN REF. 3).

### / V -> L (IN REF. 3).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CALMODULIN-BINDING (POTENTIAL).
FYN (PYRINHIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADPART) (BY SIMILARITY).
NADP (ADPART) (BY SIMILARITY).
NADP (ADPART) (BY SIMILARITY).
NASING (in isoform 3).
/FIIG=VSP_003571.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN-C57BL/6J; TISSUE-Cerebellum, Lung, and Small intestine;
MEDLINE=21085660; PubMed=1121881;
MEDLINE=21085660; PubMed=1121881;
MEDLINE=21085660; PubMed=1121881;
MEDLINE=21085660; PubMed=1121881;
MEDLINE=21085660; PubMed=1121881;
MEDLINE=21085660; PubMed=112181;
MEDLINE=21085660; PubMed=112181;
MEDLINE=21085660; PubMed=112181;
MEDLINE=21085660; PubMed=112181;
MEDLINE=21085660; PubMed=112181;
MEDLINE=21085660; PubMed=112181;
MEDLINE=2108560; PubMed
                                                                                                                                                                                                                                                        Missing (in isoform 3).
FTIG=VSP 003571.
PPISGKQSPTKNGSPEKCPRPLKVKNWETEVVLTDTLHLKS
TLETGCTEYICMGSIMHPSQHARRPEDVRTKGQLFPLAKEF
                                                                                                                                                                                                                                                                                                                                                                                         IDOYYSSIKRFGSKAHMERLEEVNKEIDTTSTYQLKDTELI
-> MRKLRITEGFGVQRGSHNHPPPQENSPPQRMAAPPSVH
ASSRSRTGRLRWFSLTPSTLRAHWKRDALSTSAWAPSCILL
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MEDLINE-98204925; PubMed-9535917;
Tonita S., Inoue N., Maeda Y., Ohishi K., Takeda J., Kinoshita T.;
Tonita S., Inoue N., Maeda Y., Ohishi K., Takeda J., Kinoshita T.;
"A homologue of Saccharomyces cerevisiae Dpmlp is not sufficient for synthesis of dollchol-phosphate-mannose in mammalian cells.";
J. Biol. Chem. 273:9249-9254(1998).
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070152; QDP829;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dolichol-Phosphate mannose synthase) (Dolichyl-phosphate beta-D-mannosyltransferase) (Mannose-P-dolichol synthase) (MPD synthase)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Pred. No. 2.5e+02;
1; Mismatches 0; Indels
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DPM1_MOUSE
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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownerein M.J., Bult C., Fletcher C., Fulite M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Sasaki H., Sato K., Schoenbach C., Saya T., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Saya T., Shipata Y., Storch K.F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., "Punctional annotation of a full-length mouse cDNA collection.";
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Dolichol-phosphate mannosyltrases (EC 2.4.1.83) (Dolichol-phosphate mannosyltrase) (Dolichyl-phosphate beta-D-mannose synthase) (Dolichyl-phosphate beta-D-mannosyltransferase) (Mannose-P-dolichol synthase) (MPD synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               -:- FUNCTION: Transfers mannose from GDP-mannose to dolichol
-:- FUNCTION: Transfers mannose from dolichol phosphate mannose (Dol-P-Man)
is the mannosyl donor in pathways leading to N-glycosylation,
glycosyl phosphatidylinositol membrane anchoring, and O-
-- CARANYIC ACTIVITY: GDP-mannose + dolichyl phosphate = GDP +
dolichyl D-mannosyl phosphate.
--- PATHWAY: Glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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-i- SIMILARITY: Belongs to the glycosyltransferase family 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.6%; Score 31; DB 1; Length 260; 83.3%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB004789; BAA25759.1; --
EMBL; AK005268; BAB23920.1; --
EMBL; AK004834; BAB23602.1; --
EMBL; AK004846; BAB25735.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.33,
Best Local Similarity 63.33,
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AL132966; CAB67653.1; -. AY039909; AAK64013.1; -. AY077674; AAL76152.1; -. AY087840; AAM65393.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S53490; S53490.
HSSP; P09651; 1HA1.
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EMBL;
EMBL;
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             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the Ewsi outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
MEDLINE-21016720; PubMed=11130713; MISCIRE W., Unseld M., MEDLINE-21016720; PubMed=11130713; MEDLINE-21016720; PubMed=11130713; MISCIRE W., Dencker W., Dencker W., Dencker W., Delseny W., Doutry M., Grivell L.A., Mache R., Puigdomenech P., Delseny W., Boutry M., Artiguenave F., Robert C., Brottier P., Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V., Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S., Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROC2_ARATH STANDARD, PRT, 342 AA.
043349; 094BT1; 09LFH2;
16-OCT-2001 [Rel. 40, Created)
110-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
29 kDa ribonucleoprotein, chloroplast precursor (RNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RBP29 OR AT3G53460 OR F4P12 160.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
euroaids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohta M., Sugita M., Sugiura M., "Three types of nuclear genes encoding chloroplast RNA-binding proteins (cp29, cp31 and cp33) are present in Arabidopsis thaliana: presence of cp31 in chloroplasts and its homologue in nuclei/Cytoplasms.", Plant Mol. Biol. 27:529-539(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

88.6%; Score 31; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPR001173; Glycoctrans 2.
Pfam; PF00535; Glycostransf 2.
Transferase; Glycostlransferase; Endoplasmic reticulum.
SEQUENCE 266 AA; 29654 MW; 4AFB37EA3AC3329D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN-cv. Columbia; TISSUE=Leaf;
MEDLINE=95201246; PubMed=7894017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF121895; AAD30975.1; -.
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RPPQGR 26
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ROC2 ARTH
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DT 16-OCT
DT 16-OCT
DT 15-MAR
DE 29 kDa
DE 20 kDB
DE 20 kD
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RAM VENTER A. D. Wagele M. PALLYCCHA A. TOPOPOS SEMINOMENE B.,

RAM RECIPELE J. SEMINETE M. SCHOOL C., BOTTER B. MANNY D. THE NOTICE STATES AND SEMINOMENE D. MONTONE A. MARKER S. MANNET B. MANNET B. MANNY D. MARKER B. MANN
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421 AA; 46373 MW; 341AD008A939ECFA CRC64;
    Pfam; PF00296; bac_luciferase; 1.
Oxidoreductase; Monooxygenase; Flavoprotein; FMN
INIT_MET 0
                                                                                                                                                                                                                                   192 RPPQGR 197
                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:2151017;
                                                                                                                                                                                           1 RPPRGR 6
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Q8R4P4;
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TRANSMEM
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TRANSMEM
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TMC2 MOUSE
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MEDLINE=95394816; PubMed=7665508;
Thibbaut D., Ratet N., Bisch D., Faucher D., Debussche L., Blanche F.;
Thibaut D., Ratet N., Bisch D., Faucher D., Debussche L., Blanche F.;
Thibaut D., Ratet N., Bisch D., Faucher D., Debussche L., Blanche F.;
The D-proline residue of pristinamycin IIB during the last step of pristinamych IIA blosynthesis."

-1. Bacteriol. 177:5199-5205(1995).
-1. FUNCTION: CATALYZES THE OXIDATION OF THE PROLINE RESIDUE OF PRISTINAMYCIN IIB (PIIB) TO PRISTINAMYCIN IIA (PIIA).
-1. COPACTOR: FWN.
-1. COPACTOR: FWN.
Pfam; PF0076; rrm; 2.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS501030; RRW; 1.
PROSITE; PS00030; RRW; NP 1; 2.
mRNA processing; RibonucleOprotein; Chloroplast; RNA-binding; Repeat; Transit peptide; Alternative splicing.
TRANSIT 65 CHIODODIAGE (ALTERNATIVE)
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95394837; PubMed=7665509; Blanc V., Lagreaux D., Didder P., Gil P., Lacroix P., Crouzet J.; Blanc V., Lagreaux D., Didder P., Gil P., Lacroix B., Crouzet J.; Cloning and analysis of structural genes from Streptomyces pristinaespiralis encoding enzymes involved in the conversion of pristinamycin IIB to pristinamycin IIB to pristinamycin IIA (PITA): PIIA synthase and NADH:riboflavin S'-Phosphate oxidoreductase."; PIIA synthase and J. Bacteriol. 177:5206-5214(1995).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last unnotation update)
Priscinamycin IIA synthase subunit A (PIIA synthase subunit A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE NTAA/SNAA/SOXA(BSZA) FAMILY OF MONOOXYGENASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCDI_TaxID=38300;
                                                                                                                                                                                                                                                                                                                                       Score 31, DB 1; Length 342;
Pred. No. 89;
1; Mismatches 0; Indels
                                                                                                                                            CHLOROPLAST (POTENTIAL).
29 KDA RIBONUCLEOPROTEIN.
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
LINKER (GLY-RICH).
                                                                                                                                                                                                                                                     Missing (in isoform 2),
/FTIG=VSP 009110.
CAC3410B72410988 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 AA
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InterPro, IPR002103; Bac_luciferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces pristinaespiralis.
                                                                                                                                                                                                                                                                                                 36007 MW;
                                                                                                                                                                                                                                                                                                                                       88.6%;
ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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1177
335
225
227
                                                                                                                                                                                                                                                                                                                 342 AA;
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                                                                                                                                                                                                                                                                                               SEQUENCE
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P54991;
                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- TISSUE SPECIFICITY: Inner ear.
-!- DEVELOPMENTAL STAGE: Expressed at low, constant levels in temporal bone from embryonic day 14 to day 1 after birth. Increases by 8 to 16-fold at day 5, 10 and 20.
-!- SIMILARITY: Belongs to the TMC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: May be required for the normal function of cochlear hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain, Inner ear, and Testis;
MEDLINE=219868; PubMed=1850618;
MEDLINE=219868; PubMed=1850618;
Arnaud D., Drury S., Mo. Yang Y., Riazuddin S., Ahmed Z.M., Naz S.,
Arnaud D., Drury S., Mo. Y., Makishima T., Ghosh M., Menon P.S.N.,
Deshmukh D., Oddoux C., Ostrer H., Khan S., Raizuddin S.,
Deininger P.L., Hampton L.L., Sullivan S.L., Battey J.F.,
Keats B.J.B., Wilcox E.R., Friedman T.B., Griffith A.J.;
"Dominant and recessive deafness caused by mutations of a novel gene,
TMC1, required for cochlear hair-cell function.";
Nat. Genet. 30:277-284(2002)
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
GLU/ASP/LYS/ARG-RICH (HIGHLY CHARGED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                             ô
   Length 421;
                                                             0; Indels
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Score 31; DB 1; I
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane cochlear-expressed protein 2.
                                                                                                                                                                                                                                                                                                                                     888 AA
                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
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   88.6%;
                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                     STANDARD;
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2244443266
2346667
24432
24432
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24432
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SQ SEQUENCE 888 AA; 101134 MW; 6D834D7987768FA7 CRC64;

Query Match
Best Local Similarity 83.3%; Pred. No. 2.38+02;
Matches 5; Conservative 1; Mismatches 0; Indels 1 RPPRGR 6 :||||| 857 QPPRGR 862

0,

Search completed: April 6, 2004, 16:08:01 Job time : 4.86916 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 6, 2004, 15:52:34 ; Search time 5.60748 Seconds (without alignments) 85.771 Million cell updates/sec Run on:

US-10-009-709-12 Title: Perfect score:

1 PPRGR 5 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
٦	30	00.		10	5878	bone morphogenetic
7	30	ö		71	2977	DNA-binding protei
М	30	00		~	3791	homeotic protein C
4	30	00	Н	N	in	
ហ	30	00	7	Н	3 AG5	virB3 protein - Ag
φ	30	90.	1	7	E72699	hetical pro
7	30	00	7	~	D72670	hypothetical prote
6 0	30	00	Н	Н	PIHUSC	salivary proline-r
σ	30	00	1	~1	B25372	salivary proline-r
10	30	00	7	~	AE2630	hypothetical prote
11	30	00	-	~	T46341	hypothetical prote
12	30	00	7	~1	A27307	ich Ch
13	30	00	7	7	A75036	ä
14	30	100.0	198	N	872709	ũ
12	30	00	-	7	S41316	, ,
16	30	00	N	~	855609	_
17	30	00	C/I	(7)	T50572	ч
18	30	00	C/I	0	A70626	_
19	30	00	CA.	~1	B87556	
20	30	00	C)	7	T49305	ica
21	30	00	N	71	A44110	ical
22	30	00	C)	~	T34836	e dehy
23	30	00	m	7	H96811	F3F9.
24	30	00	m	7	823	arate
25	30	00	m	N	654	hypothetical prote
26	30	00	m	7	3	conserved hypothet
27	30	00	m	7	~	gene M protein - r
12 B	30	00	m	C)	83	hypothetical prote
29	30	00	m	н		glycoprotein gp63

conserved hypothet histidine-rich kno	sensor histidine K conserved hypothet transcription fact	F2H15.19 protein - hypothetical prote	glycoprotein gc testis zinc finger conserved hypothet	prunin 2 precursor ethylene receptor glycoprotein gC -	hypothetical prote trophoblast endoth prunin 1 precursor
G83636 C44971	H75461 B87310 S41019	A86315 D84335	554265 JC7126 F87443	S51942 T07026 S54266	F96776 A46419 S51941
0.0	0 0 H	01 01 0	N (N K)	01 01 01	1211111
352 363	369 374 377	6 4 4 6 4 6 6 4 6 6 6 6	4 4 4 2 9 4 7 9 0	504 519 119	541 550 551
100.0	100.0	100.0	000.000.000.0000.0000.0000.0000.0000.0000	100.0 100.0	100.0
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ALIGNMENTS

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Done morphogenetic protein 1, BMP-1 splice form - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Musculus (house mouse)
C.Species: Musculus (house)
C.Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; C.Keywords: alternative splicing

Gaps ö 100.0%; Score 30; DB 2; Length 36; 100.0%; Pred, No. 17; cive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 5; Conservative

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1 PPRGR 5 g

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16 PPRGR 20

DNA-binding protein 100K chain - human (fragments) C;Species: Homo sapiens (man) C;Date: 25-Feb-1994 #sequence_revision 24-May-1996 #text_change 07-May-1999

C)Accession: S2970
R)Zhang, W.W.; Zhang, L.X.; Busch, R.K.; Farres, J.; Busch, H.
R)Zhang, W.W.; Zhang, L.X.; Busch, R.K.; Farres, J.; Busch, H.
B)Cochem. J. 290, 267-22, 1993
A;Title: Purification and characterization of a DNA-binding heterodimer of 52 and 100
A;Reference number: S29769; MUID:93176127; PMID:8439294
A;Accession: S29770
A;Residues: 1-34;35-55 <ZHA>
C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprot C;Keywords: DNA binding; heterodimer

Query Match
100.0%; Score 30; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 1 PPRGR 5 ò

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Gaps

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29 PPRGR 33

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us-10-009-709-12.rpr

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C; Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D72670
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop
A;Reference number: A72450; MUID:99310339; PMID:10382966
A, Title: Characterization of the virB operon from an Agrobacterium tumefaciens Ti plass A; Reference number: A28621; MUID:88186901; PMID:3281947
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A;Experimental source: strain X1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 15-Sep-2003
C;Accession: E72699
                                                              A,Accession: C28621
A;Molecule type: DNA
A;Molecule type: DNA
A)Cress: 1-108 <WAR->
A)Cress-references: GB:U03216; NID:g1196971; PIDN:AAA88647.1; PID:g1196974
A;Experimental source: plasmid pTlA6
C;Genetics:
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                                                                                                                                                                                                                                                                                             100.0%; Score 30; DB 1; Length 108; larity 100.0%; Pred. No. 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein APE0786 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                          C;Genetics:
A;Genome: plasmid
C;Superfamily: tumor-inducing plasmid pTiC58 virB3 protein
C;Superfamily: tumor-inducing plasmid pTiC58 virB3 protein
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Best Local Similarity 100.C
Matches 5; Conservative
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-150 «KAW»
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Best Local Similarity
Matches 5; Conserv
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                                                                                             homeotic protein Chox-4f - chicken)
C;Species: Gallus gallus (chicken)
C;Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 24-Sep-1999
C;Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 24-Sep-1999
C;Accession: C37914
R;Nohno, T; Noj; S; Koyama, E; Ohyama, K; Myokai, F; Kuroiwa, A; Saito, T; Tanig Call 64, 1197-1205, 1991
A;Fitler: Involvement of the Chox-4 chicken homeobox genes in determination of anteropost A;Reference number: A37914, MUID:91168267; PMID:1672266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C)Species: Agrobacterium tumefaciens
C)Species: Agrobacterium tumefaciens
C)Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 16-Jul-1999
C)Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 16-Jul-1999
R)Accession: S00779; C28621; C27127
R)Thompson, D.V.; Melchers, L.S.; Idler, K.B.; Schilperoort, R.A.; Hooykaas, P.J.J.
Nucleic Acids Res. 16, 4621-4636, 1988
A)Title: Analysis of the complete nucleotide sequence of the Agrobacterium tumefaciens
A)Reference number: S00777; MUID:88247765; PMID:2837739
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: D10289; NID: 9222806; PIDN: BAA01134.1; PID: d1001604; PID: 9222807;
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A; Residues: 1-108 <THO>
A; Residues: 1-108 <THO>
A; Cross-references: EMBL: X06826; NID: 939195; PIDN: CAA29974.1; PID: 939202
A; Experimental source: strain 15955, plasmid pTi15955
R; Ward, J.E.; Akiyoshi, D.E.; Regier, D.; Datta, A.; Gordon, M.P.; Nester, E.W.
J. Biol. Chem. 263, 5804-5814, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;12-68/Domain: homeobox homology <HOX>
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; Pred. No. 44;
0; Mismatches 0; Indels
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C.Species: human papillomavirus type 41
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Pred. No. 36;
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A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-100 kHIR>
A;Cross-references: EMBL:X56147
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Best Local Similarity 100.
Matches 5, Conservative
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-79 <NOH>
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salivary proline-rich phosphoprotein precursor PRH1 (allele PIF) - human C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Date: 29-Aug-1987 #sequence revision 29-Aug-1987 #text change 20-Aug-1999 C.Accession: B25372; A57868; G02562; G38355; S06153; B27307 R.Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O. J. Biol. Chem. 260, 11123-11130, 1885 April 2000 April 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary
A,Status: preliminary
A,Molecule type: protein
A,Molecule type: protein
A,Molecule type: protein
B,Mobinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
B,Ochem. J. 263, 497-503, 1989
A,Title: Primary structure and possible origin of the non-glycosylated basic proline-r
A,Reference number: S06153, MUID:90088384; PMID:2688632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: protein
A,Reddues: 17-161,0', 163-166 <8C3>
A,Experimental source: parctid gland
R;Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Blochemistry 30, 3351-3356, 1991
A;Tille: Basic proline-rich proteins from human parctid saliva: relationships of the c
A;Reference number: A38355; MUID:91190884; PMID:1849422
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A;Title: Structures of two HaeIII-type genes in the human salivary proline-rich protei
A;Reference number: A57868; MUID:86196106; PMID:3009472
                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 47-71 <HA2>
R,Schlesinger, D.H.; Hay, D.I.
R,Schlesinger, D.H.; Hay, D.I.
A,Title: Complete covalent structure of a proline-rich phosphoprotein, PRP-2, an inhib
A,Reference number: JP0106; MUID:86222916; PMID:3710693
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A;Residues: 123-166 <ROB>
C;Comment: The proposed biological functions are a highly potent inhibitor of crystal
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A;Residues: 1-166 <MAE>
A;Crose-references: GB:K03203; NID:g190483; PIDN:AAA60184.1; PID:g190484
R;Kim, H.S.; Maeda, N.
J. Biol. Chem. 261, 6712-6718, 1986
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C;Kuperfamily: proline-rich protein
C;Keywords: calcium hinding; phosphoprotein; pyroglutamic acid; saliva
C;Keywords: calcium hinding; phosphoprotein; predicted <SIG>
F;1-16/Domain: signal sequence #status experimental <PRC>
F;17-122/Product: protein A #status experimental <PRA>
F;17-46/Region: apatitic mineral binding
F;17-16/Product: PRP-3 #status experimental <PRP3>
F;12-16/Product: PRP-1 #status experimental <PRP3
F;12-16/Product: peptide P-C #status experimental <PPC>
F;127/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form)
F;24,38/Binding site: phosphate (Ser) (covalent) #status experimental
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A; Map position: 12p13.2-12p13.2
A; Introns: 22/1; 34/1
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                                                 A, Molecule type: protein
A, Residues: 17-166 < HAY>
A, Accession: S02563
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A; Residues: 17-122 < SC2>
A; Note: the authors call this protein PRP-4
R; Isemura, S.; Saitoh, E.; Sanada, K.
J. Blochem. 87, 1071-1077, 1980
A; Title: The amino acid sequence of a salivary proline-rich peptide, P-C, and its relating A; Reference number: A91954; MUD:80227634; PMID:7390979
A; Contents: peptide P-C
A; Accession: A91954
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A.Residues: 1-166 <KINA
R.Wong, R.S.C.; Bennick, A.
T. Biol. Chem. 255, 5943-5948, 1980
A.Jille: The primary structure of a salivary calcium-binding proline-rich phosphoprotein
A.Reference number: $42277; MuID:80204368; PMID:7380845
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A; Residues: 17-19, NV, 21-166 < WON>
A; Residues: 17-19, NV, 21-166 < WON>
A; Note: the amino-terminal 46 residues are involved with inhibiting hydroxyapatite forma A; Note: the amino-terminal 46 residues are involved with inhibiting hydroxyapatite forma A; Note: the A; Note: 154, 4800-4808, 1979
A; Title: The complete primary structure of a proline-rich phosphoprotein from human sali A; Contents: protein A A Accession: A92254, MUD:79173237; PMID:438215
A; Accession: A92254
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A;Residues: 123-166 <1SB>
R;Hay, D.I.; Bennick, A.; Schlesinger, D.H.; Minaguchi, K.; Madapallimattam, G.; Schluck
B;Hay, D.I.; Dennick, A.; Schlesinger, D.H.; Minaguchi, K.; Madapallimattam, G.; Schluck
B;Hitle: Jhe primary structures of six human salivary acidic proline-rich proteins (PRP-A;Reference number: S02562; MUID:89061650; PMID:3196309
                                                                                                                                                                                                                                                                                                                                                                                       Nalternate names: salivary acidic proline-rich protein PRH2 (validated) - human Nalternate names: salivary acidic proline-rich protein PRH2 (Contains PRH2 (basic proline-rich protein PRH2 (Contains: peptide P-C (basic proline-rich peptide IB-8b); proline-rich phosphoprotein C;Species: Homo sapiens (man) (Cipate 21.Mar-1981 #sequence revision 12-Apr-1996 #text change 08-Dec-2000 (Cipates 31.Mar-1981 #sequence revision 12-Apr-1996 #text change 08-Dec-2000 (Cipates 31.Mar-1981 #sequence revision 12-Apr-1996 #text change 08-Dec-2000 (Cipates 21.Mar-1981 #sequence revision 12-Apr-1996 #text change 08-Dec-2000 (Cipates 21.Mar-1981) (Cipates 200 Ill 193-1193) (Cipates 200 Ill 193-1193) (Cipates 200 Ill 193-1193) (Cipates 200 Ill 23-1193) (Cipa
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Residues: 17-46 <SCH>

Kim, H.S.; Maeda, N.

Bail. Chem. 261, 6712-6718, 1986

Title: Structures of two HaelII-type genes in the human salivary proline-rich protein

Reference number: A57868; MUID:86196106; PMID:3009472
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A;Residues: 1.166 c4MaB-
A;Cross-references: GB:K03202, NID:g190481; PIDN:AAA60183.1; PID:g190482
A;Schlesinger, D.H.; Hay, D.I.
Int. J. Pept. Protein Res. 17, 34-41, 1281
Int. J. Pept. Protein Res. 17, 34-41, 1281
A;Reference number: A91757; MUID:81191179; PMID:7228490
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A;Residuss: 17-19, 7W',21-122 <WO2>
R;Schlessinger, D;H'; Hay, DI.
in Peptides: Structure and Biological Function (Proc. Sixth Amer. Peptide Symp.), Gross
A;Title: Complete primary structure of a proline-rich phosphoprotein (PRP-4), a potent
A;Reference number: A94425
                                                                                                              PPRGR 72
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Molecule type: DNA
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C;Accession: A27307
R;Azen, E.A.; Kim, H.S.; Goodman, P.; Flynn, S.; Maeda, N.
Am. J. Hum. Gener. 41, 1035-1047, 1987
A;Title: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich
A;Reference number: A27307; MUID:88074309; PMID:3687941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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proline-rich pames: salivary acidic proline-rich protein
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 29-Aug-1997
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R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23037
                                                                                                                 2; Length 167;
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A;Molecule type: mRNA
A;Residues: 1-168 <APA>A;Residues: 1-168 <APA>A;Cessereferences: EMBL.AL137653
A;Experimental source: adult testis; clone DKFZp434B0914
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100.0%; Pred. No. 73;
iive 0; Mismatches 0
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100.0%; Score 30; DB
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches
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A;Map position: 12p13.2-12p13.2
C;Superfamily: proline-rich protein
C;Keywords: phosphoprotein
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A;Gene: Atu0440
A;Map position: circular chromosome
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A; Residues: 1-171 <AZE>
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C; Date: 11.70-2002 #sequence_revision 11.70-2002 #text_change 18.Nov-2002
C; Date: 11.70-2002 #sequence_revision 11.70-2002 #text_change 18.Nov-2002
C; Accession: AB2630
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell * Kango, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Readudes: 12-166 (*RAU)
A; Readudes: 12-166 (*RAU)
B; Robinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
Biochem. J. 263, 497-503, 1989
A; Title: Primary structure and possible origin of the non-glycosylated basic proline-rid
A; Reference number: S06153; MUID: 90088384; PMID: 2688632
A; Accession: S06153
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;Residues: 123-166 <ROB>
;Residues: 123-166 <ROB>
Maca. Hol. Kim, H.S.; Goodman, P.; Flynn, S.; Maeda, N.
M. J. Hum. Genet. 41, 1035-1047, 1987
;Title: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich proline-rich proline-rich prolines at the PRH1 locus coding for the human salivary-acidic proline-rich proline-rich prolines at the PRH1 locus coding for the human salivary-acidic proline-rich prolines at the PRH1 locus coding for the human salivary-acidic proline-rich prolines at the PRH1 locus coding for the human salivary-acidic proline-rich prolines at the PRH1 locus coding for the human salivary-acidic proline-rich prolines at the PRH1 locus coding for the human salivary-acidic prolines at the PRH1 locus coding for the human salivary-acidic prolines at the PRH1 locus coding for the human salivary-acidic prolines at the PRH1 locus coding for the human salivary-acidic prolines at the PRH1 locus coding for the human salivary-acidic prolines at the PRH1 locus coding for the human salivary-acidic prolines at the PRH1 locus coding for the human salivary-acidic prolines at the PRH1 locus coding for the human salivary-acidic prolines at the PRH1 locus coding for the human salivary-acidic prolines at the PRH1 locus coding for the human salivary-acidic prolines at the prolines at
                                                                                                                 Cross-references: GB:M13057; NID:g190511; PIDN:AAA98807.1; PID:g190512
Hay, D.I.; Bennick, A.; Schlesinger, D.H.; Minaguchi, K.; Madapallimattam, G.; Schluck
cochem. J. 255, 15-21, 1988
Title: The primary structures of six human salivary acidic proline-rich proteins (PRP-Reference number: S02562; MUID:89061650; PMID:3196309
Accession: S02562
                                                                                                                                                                                                                                                                                                                                                     Nolecule type: protein
;Residues: 47-71 <HAY>
;Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
jochemistry 30, 3351-3356, 1991
;Title: Basic proline-rich proteins from human parotid saliva: relationships of the cov
;Reference number: A38355; MUID:91190884; PMID:1849422
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AE2630
hypothetical protein Atu0440 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
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Ayîtile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
AyReference number: AB2577; MUID:21608550; PMID:11743193
AyAccession: AE2630
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100.0%; Pred. No. 71;
cive 0; Mismatches 0
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C, Keywords: phosphoprotein; saliva; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: nucleic acid sequence not shown
A,Molecule type: DNA
Residues: 17-41,'L', 43-118,'C',120-166 <AZE>
A,Cross-references: EMBL:K03203
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A;Introns: 22/1; 34/1
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Search completed: April 6, 2004, 16:16:55 Job time : 5.60748 secs
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C;Superfamily: potato leaf roll virus coat protein; potato leaf roll virus coat protein
C;Keywords: coat protein
F;1-199/Domain: potato leaf roll virus coat protein homology <COP>
                                                                                               R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: A75036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coat protein - cucurbit aphid-borne yellows virus
C;Species: cucurbit aphid-borne yellows virus
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 20-Sep-1999
                       Species: Pyrococcus abyssi
Space: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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A/Molecule type: DNA
A/Residues: 1-198 cSMI>
A/Cross-references: EMBL:U00010; NID:g466780; PIDN:AAA17073.1; PID:g466797
C/Genetics:
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R;Guilley, H.; Wipf-Scheibel, C.; Richards, K.; Lecoq, H.; Jonard, G. submitted to the EMBL Data Library, December 1993
A;Description: Nucleotide sequence of cucurbit aphid-borne yellows virus. A;Reference number: S41313
A;Accession: S41316
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Pred. No. 76;
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hypothetical protein PAB1533 - Pyrococcus abyssi (strain Orsay)
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Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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A; Residues: 1-199 <GUI>
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A;Gene: PAB1533
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Agrobacterium tumefaciens, and grobacterium tumefaciens (strain 15955).
Plasmid priA6, and Plasmid pri15955.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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Last sequence update)
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01-NOV-1988 (Rel. 09,
28-FEB-2003 (Rel. 41,
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P05352 agrobacteri
P02810 homo sapien
Q49626 mycobacteri
Q9byll homo sapien
Q02277 mycobacteri
Q9d338 mus musculu
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Biol. Chem. 254:4800-4808(1979)
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MEDLINE=80204368; PubMed=7380845;
 MEDLINE=85289325; PubMed=2993301;
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MEDLINE-79173237; PubMed-438215;
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-WAR-1989 (Rel. 10, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Salivary acidic proline-rich phosphoprotein 1/2 precursor (PRP-1/PRP-3) (PRP-2PRP-4) (PIF-F/PIF-S) (Protein A/protein C) [Contains: Peptide P-C]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                   "Analysis of the complete nucleotide sequence of the Agrobacterium tumefaciens virB operon.";
                                                                                                                                                                                                                                                                                                 tumefaciens Ti plasmid.",
J. Biol. Chem. 263:5804-5814(1988).
-!- FUNCTION: VirB proteins are suggested to act at the bacterial surface and there play an important role in directing T-DNA transfer to plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                              SEQUENCE FROM N.A.
STRAIN=15955; PLASMID=pTi15955;
MEDLINE=88247765; PubMed=2837739;
Thompson D.V., Melchers L.S., Idler K.B., Shilperoort R.A.,
Hooykaas P.J.;
                                                                                                                                                                                                                                                    Ward J.E., Akiyoshi D.E., Regier D., Datta A., Gordon M.P.,
Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 30; DB 1; Length 108; 100.0%; Pred. No. 20; ive 0; Mismatches 0; Indels
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                   "Characterization of the virB operon from an Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim H.-S., Maeda N.; "Structures of two HaelII-type genes in the human salivary proline-rich protein multigene family."; blol. Chem. 261:6712-6718 (1986).
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                                                                                                                                                                   Nucleic Acids Res. 16:4621-4636(1988).
                                                                                                                                                                                                                    PLASMID=pTiA6;
MEDLINE=88186901; PubMed=3281947;
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EMBL; J03216; AAA88647.1; -.
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InterPro, IPR007792, VirB3.
Pfam, PF05101, VirB3, 1.
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SEQUENCE 108 AA; 11760
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                NCBI_TaxID=358, 190386;
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P02810;
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Schlesinger D.H., Hay D.I.; "Complete primary structure of a proline-rich phosphoprotein (PRP-4), a potent inhibitor of calcium phosphate precipitation in human parotid
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MEDLINE-80227634; PubMed=7390979;
Isemura S., Saltoh E., Sanada K.;
"The maino acid sequence of a salivary proline-rich peptide, P-C, and its relation to a salivary proline-rich phosphoprotein C.";
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MEDLINE-86222916; PubMed=3710693;
Schlesinger D.H., Hay D.I.
"Complete covalent structure of a proline-rich phosphoprotein, PRP-2 an inhibitor of calcium phosphate crystal growth from human parotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the 6th
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J. Biol. Chem. 260:11123-11130(1985).
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Peppides: structure and biological function (Proceedings of the American peptide symposium), pp.133-136, Pierce Chemical Co., Rockford II. (1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Int. J. Pept. Protein Res. 27:373-379(1986).
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WCBI_TaxID=1769;
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Q9BYL1;
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                                -!- FUNCTION: PRP's act as highly potent inhibitors of crystal growth of calcium phosphates. They provide a protective and reparative environment for dental enamel which is important for the integrity
                                                                                                                                                                                SUBCELLUIAR LOCATION: Secreted.

FIR: Proteolytically cleaved; PRP-2, PRP-1, and PIF-S yield PRP-4, PRP-3 (protein A), and PIF-F, respectively.

POLYMORPHISM: Allele FRH1-4 is also known as PRH1 DA allele; allele PRH2-1 is also known as PR1 or protein C; allele PRH2-3 is also known as PR1'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SALIVARY ACIDIC PROLING-RICH
PHOSPHOPROTEIN 1/2.
SALIVARY ACIDIC PROLINE-RICH
PHOSPHOPROTEIN 3/4.
PHOSPHOPROTEIN 3/4.
INHIBIT HYDROXYAPATITE FORMATION, BIND
TO HYDROXYAPATITE AND CALCIUM.
PHOSPHORYLATION.
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; K03202; AAA60183.1; -.

R EMBL; M1057; AAA60184.1; -.

R EMBL; M1058; AAA98808.1; -.

R Genew; H2NC:9366; PRH1.

R Genew; H3709; -.

R MIM; 168730; -.

R MIM; 16870; -.

R MIM; 16870; -.

R MIM; 168710; -.

R MIM; 168710; -.

R MIM; 168710; -.

R MIM; 168710; -.

R Speat; Parctid gland; Phosphorylation; Signal; Polymorphism; SignAl; S
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16-0CT-2001 (Rel. 40, Last sequence update)
29-FBB-2003 (Rel. 41, Last annotation update)
49-FBB-2003 (Rel. 41, Last annotation update)
Mil222 OR B1170 (3 229)
Mycobacterium leprae.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterium.
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/FIGE-VAR 005563.
D -> N (in allele PRH2-1).
/FIGE-VAR 005564.
Q -> K (in allele PRH2-3).
/FIGE-VAR 005564.
F -> P (IN REF. 10).
N; A7DF62BF94E3C3EF CRC64;
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166 AA; 17017 MW;
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YF91 MYCLE
AC Q49626;
DT 16-OCT-2001
DT 16-OCT-2001
DT 38-FBE 2003
DE Hypotherical
GN Mil222 OR B1
OS Mycobacteriu
OC Bacteria; AC
OC Corynebacter
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                                                                                                                                                MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Cole S.T., Eiglmeier K., Parkhill J., Churcher C., Harris D.,
Mungall K., Banham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
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MEDLINE=21638749; PubMed=11780052;
MEDLINE=21638749; PubMed=11780052;
MEDLINE=21638749; PubMed=117.80162;
Jones M. P., Marthews L.H., Ashuret J. Babbage A.K., Bagguley C.L.,
Bailey J., Barlow K.F., Almetda J.P., Babbage A.K., Bagguley C.L.,
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Buck D., Burlor C.P., Blakey S.R., Bridgeman A.M., Brown A.J.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                             "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RVI591.
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                           Smith D.R., Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 20 40 POTENTIAL.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C20orf136.
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164 184 POI
198 AA; 20633 MW; 6
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PIR, S72709, S72709.
Leproma, ML1222; -.
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SEQUENCE FROM N.A.
                                                                                                       SEQUENCE FROM N.A.
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Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
A Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
Grafham D.V., Griffiths G., Garffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RAY M.P., Kimberley A.M., King A., Kolights A., Laird G.K., Johnson D.,
Kay M.P., Marthey M.M., King A., Kolights A., Laird G.K., Lawlor S.,
Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
A. Marsh V.L., Marchalingan M.A., Mullkin J.C., Nickerson T.,
Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
A. Phillimore B.J. C.T., Prathalingam S.R., Pluub R.W., Ramay H.A.,
A. Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
A. Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
A. Whitehead S.L., Whittaker P., Willey D.L., Williams S.A.,
Willing L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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MEDLINE-BCG;
MEDLINE-SQ406897; PubMed=1527058;
Mathur M., Kolattukudy P.E.;
Mathur M., Kolattukudy P.E.;
Molecular cloning and sequencing of the gene for mycocerosic acid synthase, a novel fatty acid elongating multifunctional enzyme, from Mycobacterium tuberculosis var. bovis Bacillus Calmette-Guerin.";
Mycobacterium tuberculosis var. bovis Bacillus Calmette-Guerin.";
J. Biol. Chem. 267:19388-19395 (1992).
-!- FUNCTION: PROBABLY TRANSFERS THE MYCOCEROSYL GROUP FROM MYCOCEROSIC ACID SYNTHASE TO THE HYDROXYL GROUP OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414.865.871(2001).
-!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 30; DB 1; Length 202;
; Pred. No. 38;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DF2678F090A3E946 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YMAI MYCBO STANDARD; PRT; 272 AA. 002277; 01-UTN-1994 (Rel. 29, Created) 01-UTN-1994 (Rel. 29, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Putative mycocerosyl transferase in mas 5'region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50105; SAM_DOMAIN; 1.
Hypothetical protein.
DOMAIN 118 184 SAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AL118506; CAC28315.1; -. Genew; HGNC:16129; C20orf136. InterPro; IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 202 AA; 22770 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
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Best Local Similarity luv...
5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PPRGR 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1765;
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YMA1_MYCBO
             ID PACTOR REPRESENTATION OF THE PROPERTY OF TH
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SEQUENCE FROM N. 14.

SECUENCE FROM N. 17.

REDINE=2108560; PubMed=11217851;

REMAIN=C77BL/GJ; TISUB=COLON;

RAWAI J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

RAWAWA T., Hara A., Pukunishi Y., Ronno H., Kondo S., Yamanaka I.,

RAGOCA K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

RAGOCA K., Matsuda H.A., Ashburnar M., Batalov S., Coliva H.,

Radoca K., Matsuda H.A., Ashburnar M., Pacole G., Quackenbush J.,

Rubil P., Lewis S., Matsudi F., Stutki R., Tomite M., Wagner L., Washib T.,

Rakin K., Okido II., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido II., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Blit C., Fletcher C., Fulita M., Gariboldi M.,

Brownstein M.J., Blit C., Fletcher C., Fulita M., Gariboldi M.,

Brownstein M.J., Blit C., Fletcher C., Fulita M., Gariboldi M.,

Rushim P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshiw K., Hasesgawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Hayashizaki Y.,

Hayashizaki Y.,

Hayashizaki Y.,
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MEDIINE=22388257; PubMed=12477932;
Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Strausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels
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200338, OSRIRO;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 43, Last annotation update)
60S ribosomal protein L19, mitochondrial precursor (L19mt).
MRPL19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al protein; Transferase; Transmembrane.
272 AA; 29827 MW; C91A93100B769229 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
-!- SIMILARITY: TO M.LEPRAE MASB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M95808; AAA25368.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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Hypothetical proteir
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01-OCT-1996 (Rel. 34, Created)
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PIR; S47304; S47304.
InterPro; IPR000982; Matrix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996
10-OCT-2003
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P52562;
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Matches
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sdergren E.J., Lu X., Gibbs R.A., A Willalon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Buffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smailus D.E., A Schein J.E., Jones S.J.M., Marra M.A., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Sahain J.E., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length Thuman and mouse CDNA sequences "."

Thuman and mouse CDNA sequences "."

Proc. Natl. Acad. Sci. US.A., McConondrial.

--- SUBCELLULAR LOCATION: Mitochondrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Gen. Virol. 76:593-602(1995).
-!- FUNCTION: THE M PROTEIN HAS A CRUCIAL ROLE IN VIRUS ASSEMBLY
AND INTERACTS WITH THE RNP COMPLEX AS WELL AS WITH THE VIRAL
MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 30; DB 1; Length 292; 100.0%; Pred. No. 56; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC020315; AAH20315.1; -...
EMBL; BC043921; AAH43321.1; -...
EMBL; MG1:122627; Mry13221.1; -...
MGD; MG1:122627; Mry13221.1; -...
InterPro; IPR001857; Ribosomal L19; I...
PRINTS; PR00061; RIBOSOMALL19; I...
PROSTITE; PS01015; RIBOSOMALL19; FALSE NEG.
Ribosomal protein; Mitochondrion; Transit peptide.
TRANSIT : 292 608 RIBOSOMAL L19; CHAIN : 292 608 RIBOSOMAL PROTEIN L19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=36409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2D85C99D97A59BF5 CRC64;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rinderpest virus (strain RBOK) (RDV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK018508; BAB31245.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 292 AA; 33578 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Query Match
Best Local Similarity 100.00
Best Local Similarity 5; Conservative
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VMAT RINDR
AC P41358;
DT 01-FEB-1995
DT 01-FEB-1995
DT 01-NOV-1995
DF 01-NOV-1995
DF NINGES; 85F
OC VITUSES; 85F
OC VITUSES; 85F
OC VITUSES; 85F
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MBDLINE=29156748; PubMed=1537810;
MBDLINE=29156748; PubMed=1537810;
MBDLINE=29156748; PubMed=1537810;
"Genes for tryptophan biosynthesis in the halophilic archaebacterium Haloferax volcanii: the tryppeg cluster.";
"J. Bacteriol. 174:1694.1697(1992)
-!- CATALYTIC ACTIVITY: Anthranilate + phosphoribosyldiphosphate = N-5. "phosphoribosyl-anthranilate + diphosphate.
-!- PATHMAY: Tryptophan biosynthesis; second step.
-!- SIMILARITY: Belongs to the anthranilate phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 30; DB 1; Length 335; 100.0%; Pred. No. 64;
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INTERPO. IPRO05940; Ant_phepho_trans.

InterPo. IPRO05940; Ant_phepho_trans.

InterPo. IPRO00312, Glyco_trans 3.

Pfam; PF00588; Glycos_trans 3.

Probom; PF001864; Glycos_trans 3; 1.

IGRFAMS; IGR01245; LTpD; 1.

Trypcophan blosynthesis; Transferase; Glycosyltransferase.

SEQUENCE 337 AA; 34551 MW; 13ECFAR2A0AB941E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam: PF00661; Matrix: 1.
ProDom; PD000741; Matrix: 1.
Matrix protein; Envelope protein.
SEQUENCE 335 AA; 37610 MW; B762DF12E2A06ECC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halobacterium volcanii (Haloferax volcanii).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Haloferax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Anthranilate phosphoribosyltransferase (EC 2.4.2.18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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TRPD HALVO
TRPD HAP
TRPD HAP
TRPD HAP
TRPD 10-OCT-
DE Anthrar
GN HAPD
OC Archee
OC Archee
OC Archee
OC Archee
RR SEQUENK
RR SEQUENK
RR SEQUENK
RR SEQUENK
RR HALOFE
RR HALOFE
RR HALOFE
RR GC - - - PA
CC - - - PA
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InterPro; IPR005817; Wht.
InterPro; IPR005816; Wht_grthfactor.
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EMBL; AF028702; AAC39550.1; -.
Genew; HGNC:12778; WNT9A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Quest Local Similarity 10v.v.
Sines 5; Conservative
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 PPRGR 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ŋ
                                                                                                                               NCBI_TaxID=9606;
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WNT9A OR WNT14
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WN9A MOUSE
ID WN9A MOUSE
AC QRESW2;
DT 10-0CT-2003
DT 10-0CT-2003
DT 10-0CT-2003
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=86308235; PubMed=3018284; Petrovskis E.A., Timmins J.G., Post L.E.; Petrovskis E.A., Timmins J.G., Post L.E.; J. Fet L.E.; J. J. Fet L.E.; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. .) (PUTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR 27 (POTENTIAL).
GLYCORROTEIN GR63.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIANED (GLCNAC. .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                        01-APR-1988 (Rel. 07, Created)
10-APR-1988 (Rel. 07, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
Glycoprotein GP63 precursor.
Viruses, seculorable struct (strain Rice) (PRV).
Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WN9A_HUMAN STANDARD; PRT; 365 AA. 014904; 096850; 15-UUL-1998 (Rel. 36, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Wnt-9a protein precursor (Wnt-14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; Vobeb 1; Herpes gl. Pfam, PF01689; Herpes gl. 1. Glycoprotein; Transmembrane; Signal. Signal.
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                                                                                                                                                                                                                                                              STANDARD;
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nes 5; Conserv
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                                                                               PPRGR 26
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                                                                                                                                                                                  RESULT 10
VGLI PRYNEI
ID VGLI PRYNEI
ID 01-APR
DT 01-APR
OX NGEL
OX NG
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                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                 MEDLINE=21308441; PubMed=11414706;
Saitch T., Hirai M., Katoh M.;
"Molecular cloning and characterization of WNT3a and WNT14 clustered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterProj.
Pfan, PRO110; wht; 1.
PRINTS, PRO1349; WNTPROTEIN.
SMART; SM00097; WNT1; 1.
PROSITE; PS00246; WNT1; 1.
Wht signaling pathway; Developmental protein; Glycoprotein; Signal.
SIGNAL 30 365 WNT-9A PROTEIN.
CHAIN 30 365 WNT-9A PROTEIN.
A0120 WW; IE1284D744C6A9B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
GO; GO:0007267; P:cell-cell signaling; NAS.
GO; GO:0007275; P:development; NAS.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                           in human chromosome 1442 region.";
Biochem. Biophys. Res. Commun. 284:1168-1175(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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TISSUB-PANCREALIC adenocarcinoms;

MEDLINES-928289203; PubMed=10362357;

Keane M.M., Ettenberg S.A., Nau M.M., Banerjee P., Cuello M.,

Penninger J., Lipkowitz S.;

"cbl-3: a new mammalian cbl family protein.";

"col-3: a new mammalian cbl family protein.";

"col-3: a new mammalian cbl family protein.";

-! FUNCTION: Regulator of EGFR mediated signal transduction.

-! SUBUNIT: Interacts with a restricted range of SH3 domain proteins.

-! SUBCELLULAR LOCATION: Nuclear (Potential).

-! ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBLC HUMAN STANDARD; PRT; 4.4 AA.

CBLC HUMAN STANDARD;

SUNDARS, QSYEZS, QSYEZS,

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2004 (Rel. 40, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Signal transduction protein CBL-C (SH3-binding protein CBL-C) (CBL-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM LONG).
MEDILNE-20035821; Pubmed=10571044;
Kim M., Tezuka T., Sudanoki Y., Sugano S., Hirai M., Yamamoto T.;
"Molecular cloning and characterization of a novel cbl-family gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBLC OR CBL3.
Homo sapiens (Human).
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutebria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S41019; S41019; HSSP; P24781; IXBR.
TRANSFAC; T04499; E.
Wormbep; T0764-6; E800636.
InterPro; IPR008967; P53-1ike.
InterPro; IPR008967; T-Dox.
PRINTS; PR00937; T-Dox; I.
PRINTS; P801283; T-Dox; I.
PROSITE; P801283; T-Dox 1:
PROSITE; P801284; T-Dox 1:
PROSITE; P801285; T-Dox 1:
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 279 T-BOX.
377 AA, 43232 MW; 8C409B29812A5796 CRC64;
                                          -!- SUBCELLULAR LOCATION: Nuclear (Potential). -!- SIMILARITY: Contains 1 T-box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z29443; CAA82575.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Gene 239:145-154(1999).
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SEQUENCE
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CBLC_HUMAN
        SO THE STATE OF THE SOURCE COURTS SOURCE COU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WANTAA gene cluster.";

Int. J. Mol. Med. 9:221-227(2002).

-!-FUNCTION: Ligand for members of the frizzled family of seven transmembrane receptors. Probable developmental protein. May be signaling molecule which affects the development of discrete regions of tissues. Is likely to signal over only few cell diameters (By similarly).

-!-SUBCELLUIAR LOCATION: Possibly secreted and associates with the extracellular matrix.

-!-TISSUE SPECIFICITY: Expressed in adult brain, lung, skeletal mascle, heart, and 11-day embryo.

-!-SIMIARITY: Belongs to the Wnt family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD: MGI: 2446084; Wht. String MGI: 2446084; Wht. String MGI: 2446084; Wht. InterPro; IPR005817; Wht. InterPro; IPR005816; Wht_grthfactor. Pera; PF00110; Wht. 1.
PRINTS; PR01349; WNTPROTEIN.
SMART; SM00097; WNT1; 1.
PROSITE; PS00246; WNT1; 1.
Wht signaling pathway; Developmental protein; Glycoprotein; Signal. SIGNAL 3 365 WNT-9A PROTEIN.
CARBOHYD 103 103 WNT-9A PROTEIN.
CARBOHYD 103 103 W-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning and expression of mouse Wnt14, and structural comparison between mouse Wnt14-Wnt3a gene cluster and human WNT14-
                                                                                            Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 103 N-LINKED (GLCNAC. .) (POTENTIAL) 365 AA, 40388 MW, C6EBBE1897D2FA8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 AA
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=21826279; PubMed=11836627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
            Wnt-9a protein precursor (Wnt-14) WNT9A OR WNT14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB072311; BAB84710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative T-box protein 9. TBX-9 OR T07C4.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 PPRGR 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Berks M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PPRGR 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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Q22289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
SEQUENCE
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TRESULT 13
TRA9 CAREEL
TD CA2286
DT O1-NOY
DT 10-OCT
DE PUTAT;
GN CABD-10
OC BUKAT;
OC READ:

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Gaps

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Gарв

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5; Conservative

Local Similarity

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Search completed: April Job time: 3.2243 secs
RHISN
          SWEET THE STATE OF THE STATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The state of the s
                                             -i-TISSUE SPECIFICITY: Ubiquitous.
-i-DOMAIN: The N-terminus is composed of the phosphotyrosine binding (PTB) domain, a short linker region and the RING-type zinc finger. The PTB domain, which is also called TKB (tyrosine kinase binding) domain, is composed of three different subdomains: a four-helix bundle (4H), a calcium-binding EF hand and a divergent SH2 domain. DOMAIN: The RING-type zinc finger domain mediates binding to an EZ ubiquitin-conjugating enzyme (BP similarity).
-i-PTM: Phosphorylated on tyrosines by EGFR.
-i-MISCELIAMBOUS: This protein has one functional calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHOTYROSINE (BY SIMILARITY).
Missing (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 1; Length 474; 100.0%; Pred. No. 92; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTIG=VSP 005732.
T -> N (IN REF. 2).
91013DDF12828242 CRC64;
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EF-HAND LIKE 1
EF-HAND LIKE 2
          IsoId=Q9ULV8-2; Sequence=VSP_005732;
SSUE SPECIFICITY: Ubiquitous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LINKER.
RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB028645; BAA86298.1; -. EMBL; AF117646; AAD34341.1; -. EMBL; AF117647; AAD34342.1; -. HSSP; P22661; 1B47. Genew; HGNC:15961; CBLC.
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DOMAIN
CA BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                  MEDIINES-97305956; PubMed=9163424; Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A., Pereberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A., Perret X., Molecular basis of symbiosis between Rhizobium and legumes."; Nature 387:394-401 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                            Plasmid sym pNGR234a.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 protein; Plasmid.
504 AA; 57228 MW; 63E31E487DD4CB87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 30; DB 1;
100.0%; Pred. No. 98;
ive 0; Mismatches 0;
                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 57.2 kDa protein Y4JA/Y4NE/Y4SE.
Y4JA AND Y4NE AND Y4SE.
Rhizobium sp. (strain NGR234).
504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6, 2004, 16:08:01
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: STRONG, TO FZ4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000079; AAB91713.1; -. EMBL; AE000086; AAB91785.1; -. EMBL; AE000095; AAB91845.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001584; Rve. Pfam; PF00665; rve; 1.
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
5, Conserve
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 PPRGR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSPOSASES.
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                                                                                                                                                                                                                                                                                                     NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
SEQUENCE 50
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RESULT 1
Q61356
                                                                                                                                                                                                                                                                                                                                                                                   Q63326 rattus norv
Q7uxt5 rhodopirell
Q8ztw7 probaculum
Q7upe8 rhodopirell
Q8zg3 agrobacteri
Q8zg3 agrobacteri
Q8ze4 pseudomonas
Q91tr0 tupaia herp
Q8y990 oryza sativ
Q91yi5 mus musculu
Q9yd3 aeropyrum p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q61356 mus musculu
114069 homo sapien
                                                          April 6, 2004, 15:51:34 ; Search time 18.0841 Seconds (without alignments) 87.236 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        014069
                                                                                                                                                                                                    1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                            1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q14069
Q63326
Q7UXTS
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Q7UPE8
Q82FW1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9R2G3
Q882E4
Q91TR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91YIS
Q9YDA0
Q9YDY3
Q7WJM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08M390
                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                    sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                             sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                            SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                              sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_archeap:*
                                                                                                     US-10-009-709-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                     sp_plant: *
                                                                                                                        1 PPRGR 5
                                                                                                                                              BLOSUM62
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1000.00
1000.00
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Perfect score:
                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                             Database :
                                                                                                                          Sequence:
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                                                            Run on:
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8
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8wwb8 homo sapi	Q9MA/3 NOWO SapieM Q9w199 drosophila	77618 monodelph	<u>0</u> 99ar6 tt vir	lomo sapi	91b07 vibrio par	vibrio pa	Q9ful3 oryza sativ	oryza sat	oryza sat	bradyrh	agrobac	Q9nsy3 homo sapien	OS2312 streptomyce	Q82p20 streptomyce	Q9ky47 streptomyce	Q9uz77 pyrococcus	Q82gy4 streptomyce	Q84rx3 oryza sativ	Q9fk53 arabidopsis	Q811b5 mus musculu	Q7u0s9 mycobacteri	cacambe	equine he	strepto	oryza sati		Q7xi49 oryza sativ	
Q8WWB8	Q9W199	077618	Q99AR6	Q8NH35	Q9LB07	Q87MK7	Q9FU13	Q949E3	Q8RZN8	Q89D41	QBUIGO	Q9NSY3	052312	Q82P20	Q9KY47	Q9UZ77	Q82GY4	Q84RX3	Q9FK53	Q811B5	Q7U0S9	065970	066619	Q9RKR5	01XXQ	Q9PWP2	Q7XI49	
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ALIGNMENTS

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SEQUENCE FROM N.A.
MEDLINE=95096114; PubMed=7798260;
MEDLINE=95096114; PubMed=7798260;
Takahara K., Lyons G.E., Greenspan D.S.;
Takahara K., Lyons G.E., Greenspan D.S.;
Takahara K., Lyons G.E., Greenspan D.S.;
The morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoded by alternatively spliced transcripts which are differentially expressed in some tissues.";
Takentially expressed in
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"Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
which is related to the Drosophila dorsoventral gene tolloid and
encodes a putative astacin metalloendopeptidase.";
Dev. Biol. 163:175-183(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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      36 AA
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PRT;
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MEDLINE=94229342; PubMed=8174772;
                                       O61356;
01-NOV-1996 (TrEMBLrel. 01, C:
01-NOV-1996 (TrEMBLrel. 01, L:
01-UTN-2003 (TrEMBLrel. 24, L:
BMP-1 protein (Fragment).
BMP1 OR BMP-1.
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Best Local Similarity 100.
Matches 5; Conservative
PRELIMINARY;
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Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.",
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STRAIN=INZ / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I., Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                      Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
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Thermoproteaceae, Pyrobaculum.
NCBI_TaxID=13773;
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EMBL; AE009908; AAL64642.1; -.
InterPro; IPR002792; TRAM.

Fram; PF01938; TRAM.

Hypothetical protein; Complete proteome.

SEQUENCE 79 AA; 8695 MW; B36D5871B6C30143 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
MBL; BX294134; CAD71918-1; -
Hypothetical proctein; Complete proteome.
SEQUENCE 63 AA; 6873 MW; D14BE2CD57131BD3 CRC64;
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1-MAR 2002 (TrEMBLrel. 20, Last sequence update)
01-UTN -2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PAE3058.
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Best Local Similarity 1
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-1996 (TrEMBLrel. 21, Last annotation update)
10-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Rat malic enzyme (ME) (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chodata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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J. Biol. Chem. 265:7395-7400(1990).
Biol. Chem. 265:7395-7400(1990).
Biol. Chem. 265:7395-7400(1990).
NOW TER.
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SEQÜENCE 62 AA, 6617 MW, PACGF60B9F96DD47 CRC64;
                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bonaldo M.F., Yu M.T., Telence P., Brown S., Su L., Lawton L.,
Bonaldo M.F., Yu M.T., Telence P., Brown S., Su L., Lawton L.,
Bonaldo M.F., Marburton D., Soares M.B.;
"Selection of cDNAs using chromosome-specific genomic clones:
application of chromosome 13.";
Hum. Mol. Genet. 3:1663-1673(1994).

EMBL; L33990; AAA74367.1;
NON_TER 40 40
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Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(Clone E18) gene from CpG-enriched DNA (Fragment).
Homo sapiens (Human).
                                                                                                                                                                        40 AA.
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MEDLINE=89096948; Pubmed=3211151;
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MEDLINE=90237036; PubMed=2332433;
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                                            16 PPRGR 20
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1 PPRGR 5
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SEQUENCE Query Match

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Q9R2G3;
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Q882E4
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=2147403; Pubmed=11572948;
MEDLINE=2147403; Pubmed of N. Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                              Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales, Planctomycetaceae, Pirellula.
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycinese, Streptomycinese, Streptomycetaceae, Streptomyces.

NCBI_TaxID=33903,
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Pred. No. 91;
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MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).

BMBL; BX294145; CAP7514.1; -.

Hypotherical process, Complete proteome.

SEQUENCE 82 AA; 9143 MW; 5004CB56496A2944 CRC64;
                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
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01-0CT-2003 (TrEMBLrel. 25,
01-0CT-2003 (TrEMBLrel. 25,
Hypothetical protein.
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Best Local Similarity
Matches 5; Conserv
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                                             9 PPRGR 13
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PPRGR
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Q82FW1
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Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.,
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO16865; AAO566186.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=94010218; PubMed=8405938;
Shirasu K., Kado C.I.;
Shirasu E., Kado C.I.;
Shirasu E., It plasmid VirB proteins involved in the biosynthesis of a pilin-like conjugative structure on Agrobacterium tumefaciens.";
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                            Length 105;
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                                                                                                                                                                                                   0; Indels
Nat. Biotechnol. 21:526-531(2003).

EMBL, AP005037, BAC71853.1, -
HYpothetical protein; Complete proteome,
SEQUENCE 105 AA; 11436 MW; 14E905DB7C2CA475 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF05101; VirB3; 1.
SEQUENCE 108 AA; 11760 MW; 06616D618D722BD4 CRC64;
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Last annotation update)
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Last sequence update)
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
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InterPro; IPR007792; VirB3.
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Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-UNA-2003 (TrEMBLrel. 24, VIRB3-VIRULENCE protein. Agrobacterium tumefaciens.
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Best Local Similarity 100.
Matches 5; Conservative
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Gramene; Q8W390; -. SEQUENCE 127 AA; 13877 MW; DC58A644FD437DED CRC64;
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EMBL; AC084762; AAL58249.1; -.
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Q9YDA0
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STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
Tsitrin T., Riggs P., Hsiao J., Zismann V., Blunt S., Pai G.,
VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
Salzberg S.L., White O., Fraser C.M., "Oryza sativa chromosome 3 BAC OSUNBa0013008 genomic sequence.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  Bahr U., Darai G., "Analysis and Characterization of the Complete Genome of Tupaia (Tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Beprantophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                       Length 118;
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AFESHIJT, AAKS7007.1; -
SEQUENCE 126 AA; 14152 MW. AAAAAAA
                                                                 0; Indels
  Hypothetical protein; Complete proteome.
SEQUENCE 118 AA; 12797 MW; A6612B0E53FBC341 CRC64;
                                                                                                                                                                                                                                                     Tupaia herpesvirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae.
VCBI_TaxID=10397;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative chitinase.
OSJNRA0013008.29.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                       100.0%; Score 30; DB 16;
100.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 0;
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MEDLINE=21211637; PubMed=11312357;
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Virol. 75:4854-4870(2001).
                                     Query Match
Best Local Similarity 100.
Matches 5, Conservative
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Best Local Similarity
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Q91TRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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       Length 127;
Query Match
100.0%; Score 30; DB 10; Length 1
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBJ; BCO166356; AAH16636.1; -.
MGD; MGI:1922460; 4930540G07Rik.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR000571; Znf CCCH.
Pfam; PF00642; zf-CCCH; I.
SPART; SM00356; ZnF CCH; I.
Hypochatical protein.
EQUENCE 143 AA; 15962 MW; BE668CE32FFCAB99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE1012.
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Query Match
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EMBL; APO00060; BAA79764.1; -.
                                                                                                          Gaps
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Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN=RB50 / ATCC BAA-588;
MEDLINE=22827954; PubMed=12910271;
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
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                                                                                  Length 143;
                                                                              Similarity 100.0%; Score 30; DB 17; Length 1. Similarity 100.0%; Pred. No. 1.5e+02; 5; Conservative 0; Mismatches 0; Indels
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Desulfurococcaceae, Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein, Complete proteome.
150 Aa; 16568 MW; 03A6699A3B71CD81 CRC64;
DNA Res. 6:83-101(1999).

EMBL; AP000060; BAA79997.1; -.

PIN; E72699. P72699.

FYpotherical protein; Complete proteome.

SEQUENCE 143 AA; 14821 MW; 7C7FE14DD1EB4CBE CRC64;
                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
101-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE0786.
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Last annotation update)
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Matches 5; Conserv
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Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Cardeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A., Achtnan M., Aktin R., Baker S., Basham D., Bason M., Cherevach I., Pathman H., Achtnan M., Cronin A. Davis P., Doggett J., Paltwell T., Goble A., Hamlin M., Cronin A., Davis P., Doggett J., Leather S., Moule S., Norberczak H., G'Neil S., O'Neil S., James E., Norberczak H., G'Neil S., O'Neil S., James E., Seeger K., Abarp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Annin D., Whitehead S., Barrell B.G., Maskell D.J.;
Thorparative analysis of the genome sequences of Bordetella pertussis, The Bordetella parapertussis and Bordetella bronchiseptica.";
Bordetella parapertussis and Bordetella bronchiseptica.";
Hypothetical procein; Complete proteome.

Whypothetical procein; Complete proteome.
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Job time : 19.161 secs
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Matches 5; Conservative
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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRBs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12pl3.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 24; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (STRO/) STROEMBERG N. (JOHA/) JOHANSSON I.
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                                                                 April 6, 2004, 15:29:39 ; Search time 27.9907 Seconds (without alignments) 50.472 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ABP77583 ABM53910	ABP80319 AAU54781	ABM51300	ABM51029	AAU49884	ABB15033	ABM46403	AAU53649	ABM50168	ABP09178	AAU40624	ABM37143	AAU67516	ABM64035	AAU45745	ABM42264	AAU56685
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ALIGNMENTS

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Human, PRP-1; proline-rich protein; saliva; dental caries;
chromosome 12p13.2; arginine catabolism; ammonia production; pH increase;
oral bacterium; caries prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.
                                                                                                                                                                                                                 Human saliva PRP-1 fragment (residues 104-108), SEQ ID NO:12.
AAB48782 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-1999; 99SE-00001773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stroemberg N, Johansson I;
                                                                                                                                                   (first entry)
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as disease onset or ischemic complications. An elevated level of hydrogen peroxide in plasma or whole blood and a low level in the presence of SOD is indicative of a chronic or immune compromised condition e.g. hypertension or sepais. AAY50201-Y50334 represent peptides used in the

method of the invention

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.g. indicative of the onset of an acute cardiovascular disorders,

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Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection, diabetes, stroke
                                                                                                                                                                                                                                                         Cell activation; pancreas; treatment; cardiovascular disease; trauma; inflammatory disease; autoimmune disease; archritis; diabetes; stroke; organ rejection; ischemia, Alzheimer's disease; myocardial infarction; haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina; trauma; protease inhibitor; hypertension; sepsis.
                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kistler E;
                                           100.0%; Score 30; DB 4; Length 5; 100.0%; Pred. No. 1.4e+06;
                                                               Indels
                                                                                                                                                                                                                                       Neutrophil-activating pancreatic derived peptide 79.
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                                                                  0; Mismatches
derived oligopeptides of the invention
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                                                                                                                                                                    AAY50279 standard; peptide; 6 AA.
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AAY50279
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ô ö The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's succeptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia Human, PRP-1; proline-rich protein, saliva, dental caries, chromosome 12p13.2, arginine catabolism, ammonia production, pH increase, oral bacterium, caries prevention. thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-derived oligopeptides of the invention Gaps Gaps New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries. ö . 0 Human saliva PRP-1 fragment (residues 103-108), SEQ ID NO:11 100.0%; Score 30; DB 2; Length 6; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels Length 6; Indels Query Match
100.0%; Score 30; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; AAB48781 standard; peptide; 6 AA. Claim 4; Page 24; 36pp; English. 11-MAY-2000; 2000WO-SE000930. 99SE-00001773 Stroemberg N, Johansson I; Query Match 100. Best Local Similarity 100. Matches 5; Conservative (STRO/) STROEMBERG N. (JOHA/) JOHANSSON I. WPI; 2001-031923/04 1 PPRGR 5 WO200069890-A1. PPRGR Sequence 6 AA; Sequence 6 AA; Homo sapiens. 17-MAY-1999; 09-MAR-2001 23-NOV-2000. AAB48781; AAB48781 8888888888 ò 원

cell activating compositions which involves preparing and propertion composition which involves preparing a cell activating compositions which involves preparing a cell activating composition of the produce a homogenate; (b) removing particulates from the homogenate (c) optionally incubating the resulting the homogenate and selecting fractions that exhibit cell fractionating the homogenate and selecting fractions that exhibit cell activation activity. The methods can be used for improving treatment of cutcome or reducing risk of treatment of e.g. cardiovascular disease, infinantory disease, trauma, autoimmune diseases, arthritis, organ rejection, diabetes and diabetic complications, stroke, ischemia, alterinopathy, diabetes, verous insufficiency, unstable angina or trauma. They can be used in the veterinary treatment of a non-human subject. Protease inhibitors can be used to lower cell activation resulting from these diseases and deficiencies. The detection of an elevated level of hydrogen peroxide in plasma or whole blood and in the breated level of hydrogen peroxide in plasma or whole blood and in the presence of superoxide dismutase (SOD) indicates leukocyte up regulation,

This invention describes a novel method for the use and preparation of

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1 PPRGR

Cell activation; pancreas; treatment; cardiovascular disease; trauma; inflammatory disease; autoimmune disease; arthritis; diabetes; stroke; organ rejection; ischemia; Alzheimer's disease; myocardial infarction; haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina; trauma; protease inhibitor; hypertension; sepsis. Neutrophil-activating pancreatic derived peptide 78. Schmid-Schonbein GW, Hugli TE, AAY50278 standard; peptide; 7 AA 99WO-US005247. 98US-00038894. (CELL-) CELL ACTIVATION INC. (REGC) UNIV CALIFORNIA. (first entry) (REGC) UNIV CALIFORNIA. (SCRI) SCRIPPS RES INST. WPI; 1999-580234/49. PPRGR Stoughton RB, WO9946367-A2 11-MAR-1998; 11-MAR-1999; 12-JAN-2000 16-SEP-1999 AAY50278; RESULT 셤

This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating composition comprising (a) homogeniating pancreatic tissue in buffer at particulates from the homogenate, (c) optionally incubating the resulting factoriates removed, with a protease; and (d) reactionating the homogenate and selecting fractions that exhibit cell activation activity. The methods can be used for improving treatment outcome or reducing risk of treatment of e.g. cardiovascular disease, inflammatory disease, trauma, autoimmune diseases, arthritis, organ rejection, diabetes and diabetic complications, stroke, ischemia, altohemers, who and about the veterinary treatment of a non-human subject. They can be used in the veterinary treatment of a non-human subject. Protease inhibitors can be used to lower cell activation resulting from these diseases and deficiencies. The detection of an elevated level of hydrogen peroxide dismutase (SOD) indicates leukocyte up regulation, as disease onset or ischemic complications. An elevated level of hydrogen peroxide in plasma or whole blood and in the presence of superoxide dismutase (SOD) indicates leukocyte up regulation, as disease onset or ischemic complications. An elevated level of hydrogen peroxide in plasma or whole blood and a low level in the presence of SOD is indicative of a chronic or immune compromised condition e.g. hypertension or sepsis. ANYSOZOI-YSO334 represent peptides used in the method of the invention Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection, diabetes, stroke Example 9; Page 183; 184pp; English.

ö Human, PRP-1; proline-rich protein; saliva; dental caries; chromosome 12p13.2; arginine catabolism; ammonia production; pH increase; oral bacterium; caries prevention. Gaps ., Human saliva PRP-1 fragment (residues 102-108), SEQ ID NO:10. 100.0%; Score 30; DB 2; Length 7; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels AAB48780 standard; peptide; 7 AA. Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative 0 11-MAY-2000; 2000WO-SE000930. 99SE-00001773 Stroemberg N, Johansgon I; (first entry) (STRO/) STROEMBERG N. (JOHA/) JOHANSSON I. 1 PPRGR Sequence 7 AA; WO200069890-A1 Homo sapiens. 17-MAY-1999; 09-MAR-2001 23-NOV-2000. AAB48780; AAB48780 SO ठ 셤

New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.

WPI; 2001-031923/04.

Kistler E;

Claim 4; Page 24; 36pp; English.

AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being argininerich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting theeth against caries. Sequences AAB48771-B48783 represent the PRP-1invention relates to human PRP-1-derived oligopeptides (AAB48771derived oligopeptides of the invention

Sequence 7 AA;

Gaps . 0 100.0%; Score 30; DB 4; Length 7; 100.0%; Pred. No. 1.4e+06; rive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.ve

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1 PPRGR 5 PPRGR 7

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(STRO/) STROEMBERG N.
                                  WO200069890-A1
              Homo sapiens.
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                                                                                             Human, PRP-1; proline-rich protein, saliva; dental caries;
chromosome 12p13.2; arginine catabolism; ammonia production; pH increase;
oral bacterium; caries prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, PRP-1; proline-rich protein; saliva; dental caries;
chromosome 12p13.2; arginine catabolism; ammonia production; pH increase;
oral bacterium; caries prevention.
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proline-rich proteins, useful for preventing dental caries.
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                                                                          duman saliva PRP-1 fragment (residues 101-108), SEQ ID NO:9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 30; DB 4; 1
100.0%; Pred. No. 1.4e+06;
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           AAB48779 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 24; 36pp; English
                                                                                                                                                                                                        11-MAY-2000; 2000WO-SE000930
                                                                                                                                                                                                                             99SE-00001773
                                                                                                                                                                                                                                                                                  Stroemberg N, Johansson I;
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Best Local Similarity 100...
Si Conservative
                                                                                                                                                                                                                                                  (STRO/) STROEMBERG N.
                                                                                                                                                                                                                                                            JOHANSSON I.
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                                                                                                                                         Homo sapiens
                                                     09-MAR-2001
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                                AAB48779;
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RESULT 7
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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRBs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are determinants of a person's susceptibility to dental caries. PRPs are fragments. These are metabolised by oral bacteria for mutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the plf at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-derived oligopeptides of the invention
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chromosome 12p13.2; arginine catabolism, ammonia production, pH increase,
oral bacterium, caries prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 24; 36pp; English
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11-MAY-2000; 2000WO-SE000930
                                                                      99SE-00001773
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                        (STRO/) STROEMBERG N. (JOHA/) JOHANSSON I.
                                                                                                                                                                                                                                                                                                                           WPI; 2001-031923/04
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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-derived oligopeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug
                                                                                        New oligopeptides comprising 2 arginine residues from degradation of
proline-rich proteins, useful for preventing dental caries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG93874 standard; peptide; 10 AA.
                                                                                                                                          Claim 4; Page 24; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                Stroemberg N, Johansson
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(JOHA/) JOHANSSON I
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Best Local Similarity
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Score 30; DB 4; Length 10; Pred. No. 57; 0; Mismatches 0; Indels

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The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for nutritional purposes, with certain bacterial species generating ammonia the catabolism of arginine. The peptides of the invention, being arginine-tich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the derived oligopeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; PRP-1; proline-rich protein; saliva; dental caries; chromosome 12p13.2; arginine catabolism; ammonia production; pH increase; oral bacterium; caries prevention.
relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification
                                                                                                                                                                   Gaps
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                                                                                                                              100.0%; Score 30; DB 4; Length 10; 100.0%; Pred. No. 57;
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Matches 5; Conserv
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                                                                                            Sequence 10 AA;
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PPRGR 10
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AAU01685 standard, protein, 25 AA (first entry) 18-JUL-2001 AAU01685; RESULT 11 AAU01685

Gene 28 human secreted protein homlogous amino acid sequence.

Human secreted protein, diagnosis, autoimmune disease, rheumatoid arthritis, hyperproliferative disorder; neoplasm; sunburn; cardiovascular disorder; cardiovascular disorder; cerebronascular disorder; cerebral ischaemia; angiogenesis, nervous system disorder; skin aging; Alzhelmer's disease, infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; chemotaxis; preservative; organ transplantation; tissue regeneration; food additive.

Homo sapiens.

WO200123409-A2.

05-APR-2001

26-SEP-2000; 2000WO-US026371.

99US-0155804P. 27-SEP-1999;

(HUMA-) HUMAN GENOME SCI INC

Komatsoulis GA; Rosen CA, Ruben SM,

WPI; 2001-266139/27.

Nucleic acids encoding 38 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy.

Disclosure; Page 47; 488pp; English.

AAU01641-AAU01698 represent human secreted protein amino acid, and related amino acid sequences of the invention. The human secreted protein sequences are used to prevent, treat or ameliacal condition in e.g. humans, mice, rabbits, goats, horses, cate, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to human cested proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosobent assays (BLISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. reducimmunoassays or enzyme linked immunosobent assays (BLISA). Disorders with the backovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection, viruses and thust and ocular disorders e.g. corneal infection. The polypeptides can be also be used to aid wound healing and epithelial cell proliferation, to supporting cell culture of primary tisques, to corneal infection and contact in the subpurs of primary tisques, to corneal infection or contact in the contact of primary tisques, to corneal infection or contact in the contact of primary tisques, to corneal infection or contact in the contact of primary tisques, to corneal infection or contact in the contact of primary tisques, to contact the contact in the contact of primary tisques, to contact the contact of primary tisques, to contact the contact of the contact of primary tisques, to contact the contact of the contact of primary and contact of the conta transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities

Sequence 25 AA;

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100.0%; Score 30; DB 4; Length 25; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.
Matches 5; Conservative
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22 ||||| 18 PPRGR

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AAY41484 standard; protein; 28 AA.

AAY41484;

(first entry) 02-DEC-1999

Fragment of human secreted protein encoded by gene 66.

Human, secreted protein, fusion protein, gene therapy, protein therapy, diagnosis, tissue, cancer; tumour, neurodegenerative disorder, leukaemia, developmental abnormality; foetal deficiency; blood, allergy; renal; immune system, asthma; lymphocytic disease, brain, hepatic; lymphoma; inflammation; ischaemic shock, Alzheimer's disease, restenceis; AIDS, cognitive disorder, schizophrenia; proteate; Obesity; osteoclast; thymus, osteoporosis, arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens

WO9947540-A1.

23-SEP-1999

99WO-US005804 18-MAR-1999; 98US-0078563P. 98US-0078566P. 98US-0078573P.

19-MAR-1998

98US-0078574P. 98US-0078576P. 98US-0078577P. 98US-0078579P. 98US-0078579P. 98US-008312P. 9-MAR-1998 19-MAR-1998

98US-0080314P 01-APR-1998; 01-APR-1998

(HUMA-) HUMAN GENOME SCI INC.

Yu G, Young PE, Feng P, Soppet DR; , Kyaw H, Ebner R, Lafleur DW, Olsen HS; SM, Ni J, Rosen CA, Y Endress GA, Duan RD, Moore PA; Ruben SM, Wei Y, Shi Y,

WPI; 1999-562050/47.

New isolated human genes, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

Disclosure; Page 118; 484pp; English.

This sequence represents a fragment of a secreted human protein encoded by the mucleic acid molecule detailed in the descriptor line. The gene can be used conscious detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Pc portion (e.g. AAZ24802) for increasing the stability of reflates to 95 novel genes and their fragments (nucleic acid sequences: AAZ4811-Z24907, amino acid sequences AAY41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypoptides in a sample or by determining the presence of mutations in the new polyhucleotides. Specific uses are described for each of the 95 polymucleotides, based on which tissues they are most highly expressed in (see AAZ24811 for described uses) AAYA1484
AAY AAY00658 standard; protein; 34 AA.

RESULT 14

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AAY00658;

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PPRGR

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Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breat carcinomas, colon carcinomas, leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplanias or skin proliferation and differentiation (expansion of haematopoietic stem cells proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, in wound healing, hair growth, treatment of disease cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury
                                                                                                                                                                                                                                                                                                                                                                     neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                       Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is a fragment of the human telomerase of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated vertebrate telomerase genes - used to develop products :
treating cancers or for organ regeneration, nerve cell or brain cell
growth following injury or bone marrow transplantation,
                                                                   ö
                              100.0%; Score 30; DB 2; Length 28; 100.0%; Pred. No. 1.4e+02;
                                                                0; Indels
                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                     Human telomerase protein sequence fragment.
                                                                                                                                                                                                               AAY00630 standard; peptide; 34 AA
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97US-0053018P.
97US-005329P.
97US-0054642P.
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                                                                Conservative
            Query Match
Best Local Similarity
'... 5, Conserv?
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N-PSDB; AAX18255.
                                                                                              1 PPRGR 5
                                                                                                                                2 PPRGR 6
Sequence 28 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1998;
                                                                                                                                                                                                                                                                                     26-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kilian A,
                                                                                                                                                                                                                                                   AAY00630;
                                                                                                                                                                                  RESULT 13
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This sequence encodes a fragment of a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for diagnosing cancer in a patient. The telomerase can be used for diagnosing cancer in a patient. The telomerase can skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, other skin cancers, neuroblastomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cell proliferation and differentiation (expansion of themse cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth of some of the full length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                           neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation; ss.
                                                                                                                                             Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated vertebrate telomerase genes - used to develop products itreating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation.
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100.0%; Pred. No. 1.7e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               telomerase protein sequences of the invention
                                                                                                               Telomerase protein sequence fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 11; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOSYSTEMS LLC
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                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-106060/09,
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CAMB-) CAMBIA
                                                                                                                                                                                                                                                                            WO9901560-A1.
                                                                                                                                                                                                                               sapiens.
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21-JUL-1997;
04-AUG-1997;
                                                                                26-JUL-1999
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                                                                                                                                                                                                                              Homo sapie
Synthetic.
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Gaps

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Length 34;

Query Match 100.0%; Score 30; DB 2; Length 34 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 5; Conservative 0; Mismatches 0; Indels

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PPRGR 5
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ABP62124 standard; protein; 44 AA.

ABP62124;

(first entry) 12-NOV-2002 Human secreted protein SEQ ID NO 177.

nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive, antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antiparkanatic; hepatotropic; cerbroprotective; antihlammatory; antiallergic; antidiabetic; anticonvulsant; antifungal; antiparasitic; cardidat; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.

Homo sapiens.

WO200257420-A2.

25-JUL-2002

17-JAN-2002; 2002WO-US001109.

18-JAN-2001; 2001US-0262066P.

(HUMA-) HUMAN GENOME SCI INC

Olsen H; Rosen CA, Shi Y, Moore PA, Ruben SM, Lafleur DW, Ebner R, Brewer LA;

WPI; 2002-599716/64.

New polynuclectides and polypeptides useful for diagnosing, prognosing, treating or preventing e.g. neurodegenerative, central nervous system, autoimmune, respiratory, reproductive, or inflammatory diseases or disorders.

Claim 11; Page 54; 785pp; English.

The invention relates to novel genes (ABQ92553-ABQ92607) and proteins medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune blistockers e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic RESULT 15
ABP62124
ABB62124
AB

Sequence 44 AA;

0; Gaps 100.0%; Score 30; DB 5; Length 44; illarity 100.0%; Pred. No. 2.18+02; Conservative 0; Migmatches 0; Indels Query Match Best Local Similarity Matches 5; Conser

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1 PPRGR 5

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PPRGR 10

Search completed: April 6, 2004, 16:06:42 Job time: 28.9907 secs

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PPRGR 10
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                         RESULT 2
US-09-908-322-48
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Sequence 48, Appl
Sequence 302, Appl
Sequence 235436,
Sequence 177, Appl
Sequence 177, Appl
Sequence 177, Appl
Sequence 234344,
Sequence 234344,
Sequence 231007,
Sequence 231007,
Sequence 231007,
Sequence 231007,
Sequence 231007,
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                                                                                April 6, 2004, 16:14:50 ; Search time 19.6262 Seconds (without alignments) 66.909 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/PCT_BW PUB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                 1071772
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-908-322-48

0 US-10-653-593-302

2 US-10-623-593-302

2 US-10-623-393-48

4 US-10-029-386-28348

4 US-10-047-021-177

5 US-10-047-021-177

US-10-047-599-172569

2 US-10-424-599-233-07

US-10-424-599-233-03

2 US-10-424-599-233-03
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                   1071772 seqs, 262633353 residues
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                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - protein search, using sw model
                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                            US-10-009-709-12
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Match Length DB
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Perfect score:
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                                                                                                                                                                            Sequence:
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No.
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16 30 100.0 79 12 US-10-424-599-25682 Sequence 25682, 17 30 100.0 80 12 US-10-424-599-25682 Sequence 25682, 18 30 100.0 89 12 US-10-424-599-252963 Sequence 229053, 20 100.0 89 12 US-10-424-599-272972 Sequence 229053, 20 100.0 94 12 US-10-424-599-277972 Sequence 279722, 21 30 100.0 94 12 US-10-424-599-77972 Sequence 279722, 22 30 100.0 94 12 US-10-424-599-78941 Sequence 178114, 22 30 100.0 94 12 US-10-424-599-78941 Sequence 178114, 24 30 100.0 101 12 US-10-424-599-191513 Sequence 19553, 25 30 100.0 101 12 US-10-424-599-19563 Sequence 19553, 25 30 100.0 105 14 US-10-424-599-19563 Sequence 19596, 27 30 100.0 105 14 US-10-424-599-19563 Sequence 11675, 28 30 100.0 105 14 US-10-424-599-19563 Sequence 11675, 29 30 100.0 111 12 US-10-424-599-163482 Sequence 11675, 29 30 100.0 111 12 US-10-424-599-163482 Sequence 11675, 30 100.0 111 12 US-10-424-599-163482 Sequence 11675, 30 100.0 112 US-10-424-599-163482 Sequence 11675, 30 100.0 112 US-10-424-599-163482 Sequence 27743, 30 100.0 122 12 US-10-424-599-18950, Sequence 27743, 30 100.0 122 12 US-10-424-599-22915 Sequence 27743, 30 100.0 139 12 US-10-424-599-22915 Sequence 27743, 30 100.0 139 12 US-10-424-599-22915 Sequence 27743, 30 100.0 152 12 US-10-24-499-3161 Sequence 27720, 41 30 100.0 151 12 US-10-24-599-22915 Sequence 27743, 41 30 100.0 151 12 US-10-264-761-1070 Sequence 27720, 41 30 100.0 151 12 US-10-29-299-21095 Sequence 27070, Applied 27700, Applied 27700,
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RESULT 1
US-09-572-404B-68
i Sequence 68 Application US/09572404B
i Sequence 68 Application US/09572404B
i Publication No. US203300733741
j Publication No. US203300733741
j Publication No. US203300733741
j GENERAL INCORMATION:
CURRENT PETERENTIAL Complementary peptide ligands from the human genome FILE REFERENCE: Human peener
CURRENT APPLICATION NUMBER: US/09/572,404B
i CURRENT FILING DATE: 2000-05-17
j NUMBER OF SEQ ID NOS: 4203
j SOFTWARE: PROPERENT Version 1.0
j SEQ ID NOS 60
j SEQ ID N
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Gaps
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NUMBER OF SEQ ID NOS: 470
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TILE OF INVENITON: 95 Human secreted proteins
FILE REFERENCE: PZ027P1C1
CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT APPLICATION NUMBER: US/939945
PRIOR FILING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR PLILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR PLILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-04-01
PRIOR PRILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR PRILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
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100.0%; Pred. No. 84;
trive 0; Mismatches 0;
                                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION: UNKnown>
PRIOR APPLICATION NUMBER: 08/981,392
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT TROCRAFION:
REGISTRATION: NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 32,605
TELERPANC: 212-790-9090
TELERPAX: 212-869-8864
TELERPAX: 212-869-8864
TELERAX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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Matches 5; Conserva
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0
                Gray, Grace
TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 12;
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10S-09-783-931-48
1 Sequence 48, Application US/09783931
2 Publication No. US20030073620A1
1 GENERAL INFORMATION:
1 Henrique, Domingos Manuel Pinto
1 Lewis, Julian Hart
2 Artavanis-Teakonas, Spyridon
3 Artavanis-Teakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 30; DB 9;
100.0%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTHARE: FASLSGQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATA:
APPLICATION NUMBER: 08/09/908,322
APPLICATION NUMBER: 08/09/908,322
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/091,392
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
  Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLGGY: withown MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 48: US-09-908-322-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
TELEPHONE: 212-790-9090
TELEEX: 212-869-864
TELEX: 66.41 PENNE
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity 100.
Matches 5; Conservative
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Gaps
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                           Indels
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100.0%; Pred. No. 2.6e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.

TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: P2016F1
CURRENT APPLICATION NUMBER: US/10/411,224
CURRENT FILING DATE: 2003-04-11
FRICR APPLICATION NUMBER: US/09/722,329
FRICR APPLICATION NUMBER: US/09/722,329
FRICR APPLICATION NUMBER: 09/262,109
FRICR FILING DATE: 1997-09-05
FRICR APPLICATION NUMBER: 60/057,626
FRICR FILING DATE: 1997-09-05
FRICR APPLICATION NUMBER: 60/057,663
FRICR APPLICATION NUMBER: 60/057,663
FRICR APPLICATION NUMBER: 60/057,669
FRICR FILING DATE: 1997-09-05
FRICR APPLICATION NUMBER: 60/059,67
FRICR FILING DATE: 1997-09-12
FRICR APPLICATION NUMBER: 60/058,667
FRICR APPLICATION NUMBER: 60/058,973
FRICR APPLICATION NUMBER: 60/058,973
FRICR APPLICATION NUMBER: 60/058,973
FRICR FILING DATE: 1997-09-12
FRICR FILING DATE: 1997-09-12
FRICR FILING DATE: 1997-09-12
FRICR APPLICATION NUMBER: 60/058,666
FRICR FILING DATE: 1997-09-12
FRICR APPLICATION NUMBER: 60/050,112
FRICR FILING DATE: 1997-09-12
FRI
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                    Mismatches
                                                                                                                                                                                                                                                                                                     Sequence 177, Application US/10411224
Publication No. US20030166906A1
GENERAL INFORMATION:
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                    5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                            24 PPRGR 28
                                                                                  1 PPRGR 5
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                    Matches
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Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
ITILE OF INVENTION: HUMAN GROWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-x-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 28348
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 235436, Application US/10424599
Sequence 235436, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vondie S
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILLE REFERENCE: 38-21(5323)B
CURRENT APPLICANTION: PLANTS RUG/10/424,599
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 235436
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OTHER INFORMATION: MAP TO CHR22 126.0
OTHER INFORMATION: EXPRESSED IN PRACENTA, SIGNAL = 0.33
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.49
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
US-10-029-386-2834TEND
                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 30; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                   Score 30; DB 12;
Pred. No. 1.8e+02;
                                                                                                                                                                0; Mismatches
                                                                                               100.0%;
                                                                                        Query Match
Best Local Similarity 100.
Matches 5, Conservative
; ORGANISM: Homo sapiens
US-10-653-595-302
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: East Thomas J
APPLICANT: Alou Struct
APPLICANT: Alou Struct
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 172569
LENGTH: 51
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN ADULI LIVER, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEALL LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEALL SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEALL, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEALL SIGNAL = 1.2
OTHER INFORMATION: EXT.HUMAN HIT: PROSIG, EVALUE 4.00e+00
US-09-864-761-40999
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US-10-424-599-172569
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOPTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 40999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 172569, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 PPRGR 15
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US-10-424-599-238344
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US-10-424-599-172569
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Sequence 40999 Application US/09864761

Patent No. US20020040763A1

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Homeward GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEPUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-06-04

PRIOR PILING DATE: 2000-06-05

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-09-07

PRIOR PILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PILING DATE: 2000-09-07

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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; Pred. No. 2.6e+02;
0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
         PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/057,663
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 60/058,974
PRIOR APPLICATION NUMBER: US 60/058,973
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 206
SEQ ID NO 177
LENGTH: 44
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APPLICATION NUMBER: PCT/USO1/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
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CAGANISM: Homo sapiens
US-10-047-021-177
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Best Local Similarity
Matches 5; Conserv
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US-09-864-761-40999
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Sequence 204887, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La ROSA Thomas J
APPLICANT: La ROSA Thomas J
APPLICANT: ANO Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 204287
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OP SEQ ID NOS: 285684
EBO ID NO 223703
LENGTH: 72
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_50620C.1.pep
US-10-424-599-231007
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CTHER INFORMATION: Clone ID: PAT_MRT3847_26499C.1.pep

US-10-424-599-204287
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                                                                                                                                                             NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 231007
LENGTH: 67
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ORGANISM: Glycine max
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US-10-424-599-223703
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us-10-009-

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Avoralic David K
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 238344
LENGTH: 63
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| Publication No. US20040031072A1
| GENERAL INFORMATION No. US20040031072A1
| GENERAL INFORMATION No. US20040031072A1
| GENERAL INFORMATION NO. US20040031072A1
| APPLICANT: La ROSa Thomas J
| APPLICANT: Chou Yihua
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF THING DATE: 2003-4-28
| CURRENT FILING DATE: 2003-4-28
| CURRENT FILING DATE: 2003-4-28
| SEQ ID NO 277753
| LENGTH: 65
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: About K
APPLICANT: Cov Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICANTON WUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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100.0%; Score 30; DB 12; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels.
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US-10-424-599-277753
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US-10-424-599-238344
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ORGANISM: Glycine max
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US-10-424-599-277753
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US-10-424-599-231007
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Query Match 100.0%; Score 30; DB 12; Length 72; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 5; Conservative 0; Mismatches 0; Indels 1 PPRGR 5 |||||| 29 PPRGR 33 ò

Search completed: April 6, 2004, 17:06:09 Job time : 20.6262 secs

-09-436-9B3-6

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Query Match
Best Local Similarity 100.
Matches 5; Conservative
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 2233437
2233437
319883, A
2119889, A
1188283, A
1188283, A
2888019, A
29848, A
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29, Appl
21850, A
24990, A
21451, A
23646, A
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17072, A
27105, A
7, Appli
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29505, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 48, App.
                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                      6, 2004, 15:56:34 ; Search time 7.33645 Seconds (without alignments) 35.185 Million cell updates/sec
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. /cgn2 6/ptodata/2/iaa/5A_COMB.pep:*
. /cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
. /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
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. /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
. /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-252-991A-2343
US-09-252-991A-22741
US-09-252-991A-31969
US-09-252-991A-31969
US-09-252-991A-31988
US-09-252-991A-18283
US-09-252-991A-18283
US-09-252-991A-18283
US-09-252-991A-18419
US-09-252-991A-29886
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US-08-559-377A-11
US-02-252-991A-17072
US-09-252-991A-27105
US-09-436-983-7
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US-09-252-991A-21850
US-09-252-991A-24990
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US-09-252-991A-23646
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Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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1 PPRGR 5
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Perfect score:
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No.
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APPLICANT: Ish-Horowicz, David
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Argance
TILLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES, 94
CORRESPONDENCE ADDRESS;
ADDRESSEE: Pennie & Edmonds LLP
STREET: 11.55 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: UGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Sequence 6, Appli
Patent No. 5223425
Sequence 21942, A
Sequence 25956, A
Patent No. 5223425
Sequence 16625, A
Sequence 16625, A
Sequence 16625, A
Sequence 17429, A
Sequence 27429, A
Sequence 25333, A
Sequence 21798, A
Sequence 21798, A
Sequence 21798, A
Sequence 21798, A
Sequence 22333, A
Sequence 22333, A
Sequence 22333, A
Sequence 22533, A
Sequence 22532, A
Sequence 21743, A
Sequence 21743, A
Sequence 21533, A
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                                                                                   US-09-252-991A-25956

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US-09-252-991A-28573

US-09-252-991A-14069

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US-09-252-991A-32247

US-09-252-991A-32247

US-09-252-991A-32247

US-09-252-991A-32247

US-09-252-991A-3237

US-09-252-991A-2333

US-09-252-991A-2333

US-09-252-991A-2333

US-09-252-991A-2333
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ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
COMPUTER: IBM COMPUTER:
COMPARIBLE: 22-DEC-197
CLASSIFICATION NUMBER: US/08/981,392
REPERNICE/DOCKET NUMBER: 7326-038
REGISTRATION NUMBER: 32,605
REGISTRATION NUMBER: 32,605
RECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEMOTH: 12 amino acids
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDENDES:
TOPOLOGY: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
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Patent No. 6262025
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4. Application US/08454730;
Sequence 1. Application US/08454730;
Patent No. 5789177;
GENERAL INFORMATION:
APPLICANT: Rijeswijk, Franciscus Antonius Maria
APPLICANT: Rijeswijk, Franciscus Antonius Maria
APPLICANT: Maes, Roger Kamiel
TILLE OF INVENTION: Bevine Herpesvirus Type 1
TITLE OF INVENTION: Deletion Mutants, Vaccines Based
TITLE OF INVENTION: Delection Of Bovine Herpesvirus
TITLE OF INVENTION: Thereon, Diagnostic Kits For
TITLE OF INVENTION: Type 1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                     0; Mismatches
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APPLICATION NUMBER: US/08/454,730
FILIND DATE: MAY 31, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/150,203
FILIND DATE: December 6, 1993
ATTORNEY/AGENT INFORMATION:
NAME: ROMAID J. BAYON
REGISTATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 29,281
REFERENCE/GOCKET NUMBER: 29,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch,
MEDIUM TYPE: 1.44 MB Storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WORD PERFECT 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jericho
New York
Y: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Hoffmann & Baron
350 Jericho Turnpike
TELEPHONE: (516) 822-3550
IELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
     (516) 822-3550
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Best Local Similarity 100.0
Matches 5; Conservative
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TOPOLOGY: Lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 35
                                                                                                                                                                                                                US-08-150-203A-4
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                                                                                                                                                                         Sequence 30895, Application US/09252991A

Patent No. 5551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:

FILE REPERENCE: 107196.136

CURRENT PELLING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PELING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LIENGTH: 81

LIENGTH: 81
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APPLICANT: Rijsewijk, Franciscus Antonius Maria
APPLICANT: van Oirschot, Johannes Theodorus
APPLICANT: Rose, Roger Kamiel
TITLE OF INVENTION: Bovine Herpesvirus TITLE OF INVENTION: Detection Of Bovine Herpesvirus
TITLE OF INVENTION: Type 1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: HOffmann & Baron
STREET: 350 Jericho Turnpike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: New Tolk COUNTRY: United States of America 21P: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, MEDIUM TYPE: Diskette - 3.5 inch, MEDIUM TYPE: 1.44 MB Storage COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS DOS SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,203A FILING DATE: December 6, 1993
CLASSIFICATION 435
PRIOR APPLICATION DATA: NO. 5676951E ATTORNEY AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37, 133
REFERENCE/DOCKET NUMBER: 294-22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York : United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT / ORGANISM: Pseudomonas aeruginosa US-09-252-991A-30895
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Best Local Similarity 100.
Matches 5; Conservative
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                                               5 PPRGR 9
  1 PPRGR 5
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; TYPE: PRT; ORGANIEM: Pseudomonas aeruginosa US-09-252-991A-23673
                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
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US-09-252-991A-23673
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
FILLE REPERENCE: 107196.113 6
CURRENT APPLICANTON NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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100.0%; Pred. No. 82;
tive 0; Mismatches 0; Indels
                                                                           APPLICANT: Wisewijk, Franciscus Antonius Maria
APPLICANT: van Oirschot, Johannes Theodorus
APPLICANT: Maes, Roger Kamiel
TITLE OF INVENTION: Bovine Herpesvirus Type 1
TITLE OF INVENTION: Delection Mutants, Vaccines Based
TITLE OF INVENTION: Detection Of Bovine Herpesvirus
TITLE OF INVENTION: Type 1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
                                                                                                                                                                                                                                                                                                                      STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COMPUTRY: United States of America
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch,
MEDIUM TYPE: 1.44 MB Storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: 08/150,203
FILING DATE: 22-WAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Louise A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 294-22
TELECOMMUNICATION INFORMATION:
           Sequence 4, Application US/08949788 Patent No. 6403097
                                                                                                                                                                                                                                                                                                        B: Hoffmann & Baron
350 Jericho Turnpike
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INFORMATION POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
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Best Local Similarity 100.
Matches 5, Conservative
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                                                               GENERAL INFORMATION:
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US-09-252-991A-23343
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-08-949-788-4
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Sequence 23673, Application US/09252991A

Sequence 23673, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 142
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APPLICANT: MARC J. RUBERTIEL GLE A 1.
APPLICANT: MARC J. RUBERTIEL ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: APPLICATION OF SEQUENCES AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.236
FILE REPERENCE: 107196.218
PRIOR FILING DATE: 1999-02-18
PRIOR PLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1999-02-18
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100.0%; Score 30; DB 4; Length 13
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 23343
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; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21773
LENGTH: 165
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Patent No. 6551795
Fatent No. 6551795
Fatent No. 6551795
FATENCE INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
FILE REPERRNCE: 107196.136
CURRENT FILING DATE: 1099-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILLE REPERENCE: 107196.136

FILLS REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRICR APPLICATION NUMBER: US 60/074,788

PRICR FILING DATE: 1998-02-18

PRICR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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// Patent No. 6551795
// GENERAL INFORMATION:
Sequence 21773, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18283
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LENGTH: 172
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PRICANT:
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Parent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PAPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
FRICK RILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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100.0%; Score 30; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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    Query Match 100.0%; Score 30; DB 4; Length 142; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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US-09-252-991A-31988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31989
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Best Local Similarity
Matches 5; Conserv
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US-09-252-991A-21773
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                Matches
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Sequence 28848, Application US/09252991A

Sequence 28848, Application US/09252991A

Patent No. 6551795

GENERAL INPORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLECC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: NUCLECC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

FILE REFERENCE: 107196.136

CURRENT PFLING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGENCE 28806, Application US/09252911A
PRETENT NO. 5551795
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107136.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28806
LENGTH: 175
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                                                                                                                                                                                                               Length 172;
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100.0%; Score 30; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                             100.0%; Score 30; DB 4; I
100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                           0; Mismatches
       60/094,190
                                                                                                                 TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28806
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29848
PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 18419
                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                      1 PPRGR 5
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US-09-252-991A-28806
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OM protein - protein search, using sw model

Run on:

April 6, 2004, 15:52:34; Search time 19.0654 Seconds (without alignments) 85.771 Million cell updates/sec

US-10-009-709-13 Title: Perfect score:

104 1 GGHPRPPRGRPQGPPQQ 17 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

elki protein - mou hymothetical arote	HBF-GENCATOR PLOCE PDF-3-3-2-3-1-3-1-3-1-3-1-3-1-3-1-3-1-3-1-3	hypothetical prote	broline-rich prote	proline-rich prote	proline-rich prote	proline-rich prote	cholecystokinin B	cholecystokinin B	protein kinase (EC	hypotherical prote	1184714 A - Califo	eyelid - fruit fly
JC4965 J26427	T37451	T10340	C29149	B24264	A24264	S22373	S48049	A46195	JC4070	T26656	T08852	T13049
20	~ ~	1010	1 (1	C)	N	~	N	~	Н	N	N	(3
429 646	469	875	227	240	240	260	381	452	543	1384	1428	2715
51.9	51.0	51.0	50.5	50.5	50.5	50.5	50.0	50.0	50.0	50.0	49.5	49.5
75 72 4 44		53	52.5	52.5	52.5	52.5	52	25	52	52	51.5	51.5
30	332	8 c 4 c	36	37	38	ტ ტ	0.4	41	42	43	44	45

ALIGNMENTS

		in precursor PR
		salivary proline-rich phosphoprotein
		salivary proline-rich phospho
RESULT 1	PIHUSC	salivary

RH2 [validated] - human

NALTETINGE DESIGNOPTORED PROCUESOR PRIZE [Validated] - human NALTETINGE STATES AND SEPTION PROPERTY AS A VALUE TO PROPERTY AS A VALUE AND A VALUE TO PROPERTY AND A VALUE A

A; Molecule type: DNA
A; Residues: 1.166 (KINA)
A; Residues: 1.166 (KINA)
A; Cross-references: GB: M.13058; NID:g190513; PIDN:AAA98808.1; PID:g190514
R; Worg, R.S.C.; Bennick, A.
J. Biol. Chem. 255, 5943-5948; 1980
A; Title: The primary structure of a salivary calcium-binding proline-rich phosphoprote.
A; Reference number: A92277; MUID:80204368; PMID:7380845
A; Contents: protein
A; Accession: A92277; MUID:80204368; PMID:7380845
A; Accession: A92277; MUID:80204368; PMID:7380845
A; Residues: 17-19; VX, 21-166 < WON>
A; Residues: 17-19; VX, 21-166 < WON>
A; Residues: L7-19; VX, 21-166 < WON>
A; Note: the amino-terminal 46 residues are involved with inhibiting hydroxyapatite forn R; Worg, R.S.C.; Hofmann, T.; Bennick, A.
Biol. Chem. 254, Hofmann, T.; Bennick, A.
J. Biol. Chem. 254, Hofmann, T.; Punick, A.
A; Reference number: A92254; MUID:79173237; PMID:438215
A; Contents: protein
A; Reference number: A92254; MUID:79173237; PMID:438215
A; Contents: protein
A; Accession: A92254; MUID:79173237; PMID:438215

A; Accession: A92254

synaptobrevin - lo

A,Molecule type: protein A,Residues: 17-19,'N',21-122 <WO2> R;Schlessinger, D.H.; Hay, D.I. in Peptides: Structure and Biological Function (Proc. Sixth Amer. Peptide Symp.), Gros: A;Title: Complete primary structure of a proline-rich phosphoprotein (PRP-4), a potent A;Reference number: A94425

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A,Molecule type: protein
A,Residues: 47-71 «HAY»
R;Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Biochemistry 30, 3351-3356, 1991
A;Hile: Basic proline-rich proteins from human parotid saliva: relationships of the can A;Reference number: A38355; MUID:91190884; PMID:1849422
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A, Residues: 123-166 (*ROB>
A, Residues: 123-166 (*ROB>
R; Azen, E.A.; Kim, H.S.; Goodman, P.; Flynn, S.; Maeda, N.
Am. J. Hum. Genet. 41, 1035-1047, 1987
A, Titlle: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich p
A; Reference number: A27307; MUID:88074309; PMID:3687941
A; Concents: allele Pa
                                          C;Species: Homo sapiens (mān)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Aug-1999
C;Accession: B25372; A55868; S02562; G38355; S06153; B27307
K;Maded, N.; Kim, H.S.; Azen, E.A.; Smithies, O.
J. Biol. Chem. 260, 11129-11130, 1985
A;Title: Differential RNA splicing and post-translational cleavages in the human saliv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference: "1-166 cAME>
A; Cross-references: GB:KO3202; NID:g190483; PIDN:AAA60184.1; PID:g190484
A; Cross-references: GB:Kim, H.S.; Maeda, N.
B; Kim, H.S.; Maeda, N.
J. Biol. Chem. 251, 6712-6718, 1986
A; Title: Structures of two HaeIII-type genes in the human salivary proline-rich protein
A; Title: Structures of two HaeIII-type genes in the human salivary proline-rich protein
A; Reference number: A57868; MUID:86196106; PMID:3009472
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A; Residues: 1-166 <KIM>
A; Residues: 1-166 <KIM>
A; Residues: 1-166 <KIM>
A; Cross-references: GBN 3057; NID:G190511; PIDN:AAA98807.1; PID:G190512
A; Cross-references: GBN 3057; NID:G190511; Minaguchi, K.; Madapallimattam, G.; Schlus Biochem. J. 255, 15-21, 1988
Biochem. J. 255, 15-21, 1988
A; Title: The primary structures of six human salivary acidic proline-rich proteins (PR A; Reference number: S02562; MUID:89061650; PMID:3196309
A; Accession: S02562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: protein
A,Residues: 123-166 <KAU>
R,Residues: 123-166 <KAU>
R,Rebinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
Bjochem. J. 263, 497-503, 1989
A,Title: Primary structure and possible origin of the non-glycosylated basic proline-r
A,Reference number: S06153; MUID:90088384; PMID:2688632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
proline-rich phosphoprotein precursor PRH1 (allele PIF) - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 104; DB 2;
ilarity 100.0%; Pred. No. 1.1e-05;
Conservative 0; Mismatches 0;
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A,Map position: 12p13.2-12p13.2
A,Introns: 22/1, 34/1
C;Superfamily: proline-rich protein
C;Keywords: phosphoprotein; saliva; tandem repeat
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A;Molecule type: DNA
A;Residues: 17-41,'L', 43-118,'C',120-166 <AZE>
A;Cross-references: EMBL:K03203
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nes 17; Conserv
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A, Residues: 1-166 < MAI
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C;Keywords: calcium binding; phosphoprotein; pyroglutamic acid; saliva
C;Keywords: calcium binding; phosphoprotein; pyroglutamic acid; saliva
E;17-16/Domain: signal sequence #status predicted <SIG>
F;17-16/Product: protein C #status experimental <PRA>
F;17-122/Product: protein A #status experimental <PRA>
F;17-46/Region: apatitic mineral binding
F;17-12/Product: pptide p-C #status experimental <PPC>
F;123-16/Product: pptide P-C #status experimental <PPC>
F;123-16/Product: pptidione carboxylic acid (Gln) (in mature form) #status experiment F;24,38/Binding site: phosphate (Ser) (covalent) #status experimental
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Molecule type: protein
Residues: 123-166 «KAU»
Robinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
Robinson, R.; Kauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
Robinson, P. Stauffman, D.L.; Waye, M.M.Y.; Blum, M.; Bennick, A.; Keller, P.J.
Robinson, R.; Kauffman, B.J.
Robinson, R.; Keller, B.J.
Robinson, R.; Robinson, R
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A,Residues: 17-161,0', 163-166 <SC3>
A,Experimental source: parotid gland
A,Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Biochemistry 30, 3381-3356, 1991
Biochemistry 30, 3381-3356, 1991
A,Reference number: A38355; MUID:91190884; PMID:1849422
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nt. J. Pept. Protein Res. 27, 373-379, 1986
Title: Complete covalent structure of a proline-rich phosphoprotein, PRP-2, an inhibit
Reference number: JP0106; MUID:86222916; PMID:3710693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 123-166 <1SB>
R;Hay, D.I.; Bennick, A.; Schlesinger, D.H.; Minaguchi, K.; Madapallimattam, G.; Schluck
Biochem. J. 255, 15-21, 1988
A;Title: The primary structures of six human salivary acidic proline-rich proteins (PRP-A;Reference number: S02562; MUID:89061650; PMID:3196309
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Residues: 123-166 <ROB>
Comment: The proposed biological functions are a highly potent inhibitor of crystal
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                               A,Accession: A94425
A,Adlecule type: protein
A,Residues: 17-122 <8C2>
A,Note: the authors call this protein PRP-4
A,Note: the authors call this protein PRP-4
B, Isemura, S.; Saltoh, E.; Sanda, K.
J. Biochem. B7, 1071-11077, 1980
A,Title: The amino acid sequence of a salivary proline-rich peptide, P-C, A,Reference number: A91954; MUID:80227634; PMID:7390979
A,Accession: A91954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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Molecule type: protein Residues: 47-71 <HA2>

Accession: JP0106

Accession: G38355

Molecule type: protein; Residues: 17-166 < HAY> Accession: S02563 A; Introns: 22/1; 34/1

Conservative

Query Match Best Local Similarity Matches 17; Conserv

115

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RESULT 2 B25372

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us-10-009-709-13.rpr

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A; Molecule type: DNA
A; Residues : 35-183,245-392
A; Cross-references: EMBL:X07516
B; Kauffman, D.; Hofmann, T.; Bennick, A.; Keller, P.
B; Molemistry 25, 238-2382, 1986
A; Title: Basic proteins from human parotid saliva: complete covalent strustations and a paroteins from human parotid saliva: complete covalent strustances: LOSS 1986
A; Title: Basic protein A; Molecule type: Drotein A; Molecule type: Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Cross-references: GDB:119511, OMIM:180989
A/Map position: 12p13.2-12p13.2
A/Rorss-references: GDB:119511, OMIM:180989
A/Map position: 12p13.2-12p13.2
A/Note: each of the tandem repeats contains a candidate splice acceptor site, and seve A/Note: each of the tandem repeats contains
C/Superfamily: proline-rich protein
C/Keywords: alternative splicing; duplication, parotid gland; phosphoprotein; pyroglut.
F):1-6/Domain: signal sequence #status predicted <SIG.
F):1-5/Product: basic proline-rich peptide FB-1 #status experimental <PBD-5/2-152/Product: basic proline-rich peptide FB-6 #status experimental <PBC-5/392/Product: basic proline-rich peptide FB-6 #status experimental <PBC-5/392/Product: basic proline-rich peptide FB-H #status experimental <PBC-5/392/Product: basic proline-rich peptide FB-H #status experimental <PBC-5/392/Product: basic proline-rich peptide B-H #status experimental <PBC-5/4/Binding site: phosphate (Ser) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 22-127, "R' 129-148, "R', 150-152 <KA3>
R;Isemura, S.; Saitch, "E.; Sanada, K.
J. Blochem. 91, 2067-2075, 1982
A;Title: Fractionation and characterization of basic proline-rich peptides of human pa. A;Reference number: A91966; MUID:83007119; PMID:7118863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: protein
A,Residues: 92-127,'R',129-148,'R',150-152 <ISE>
C;Comment: This peptide contains 21-residue repeats, two of which have internal 7-resid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              saliva: complete covalent stru
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A,Molecule Vype: DNA
A,Residues: 35-39, P',41-84,'G',86,'R',87-154,'R',218-246;300-306,'T',308-329,'C',331-
A,Accession: A05262
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R;Kauffman, D.; Wong, R.; Bennick, A.; Keller, P.
Biochemistry 21, 6558-6562, 1982.
A;Title: Basic proline-rich proteins from human parotid saliva: A;Reference number: A90464; WUID:83101329; PMID:6924859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 392,
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A; Residues: 'S', 338-392 < SAI>
R; Azen, E.; Lyons, K.M.; McGonigal, T.; Barrett, N.L.; C
Proc. Natl. Acad. Sci. U.S.A. 81, 5561-5565, 1984
A; Reference number: A94005; MUID:84298176; PMID:6089212
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0.43;
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Pred. No. 0.43;
2; Mismatches
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61.9%; Pred
2; h
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Best Local Similarity
Matches 13; Conserv
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                                                                                  R.Azen, E.A.; Kim, H.S.; Goodman, P.; Flynn, S.; Maeda, N.
Am. J. Hum. Genet. 41, 1035-1047, 1987
A.Title: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich prd
A.Reference number: A27307; MUID:88074309; PMID:3687941
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A; Residues: 1-183,245-392 <MAE>
A; Residues: 1-183,245-392 <MAE>
A; Cross-references: GB: K03204; NID: g190485; PIDN: AAA60185.1; PID: g190486
A; Note: alternatively splice forms lacking portions of the repeat region were also found
R; Lyons, K.M.; Stein, J.H.; Smithies, O
R; Lyons, K.M.; Stein, J.H.; Smithies, A; Title: Length polymorphisms in human proline-rich protein genes generated by intrageni
A; Reference number: S02127; MUID: 89121440; PMID: 2851479
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A, Note: authors translated the codon CAA for residue 272 as Arg
A, Note: authors translated the codon CAA for residue 272 as Arg
R, Madda, N., Kim, H.S., Azen, E.A.; Smithies, O.
J. Biol. Chem. 260, 11129-11130, 1985
A, Titlel Differential RNA splicing and post-translational cleavages in the human salivar A, Reference number: A92492, MUID:85289325; PMID:2993301
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A; Modecule type: DNA
A; Residues: 35-127, 'K',129-148,'R',150-151,153-187,'K',189-272,'S',274-336,'S',338-392
A; Cross-references: GB:S62929
A; Experimental source: subject M.V.O. (large allele)
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C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 29-Aug-1997
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A;Residues: 35-127,250-273,'R',275-277,'R',279-336,'S',338-392 <LYO>
A;Cross-references: EMBL:X07517
A;Accession: S02127
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Pred. No. 1.1e-05;
; Mismatches 0;
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Cross-references: GB:S62941
Experimental source: subject C.J. (large allele)
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Residues: 35-183,245-270,'Q',272-392 <AZ3>
Cross-references: GB:S62928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:119515; OMIM:168730
A;Map position: 12p13.2-12p13.2
C;Superfamily: proline-rich protein
C;Keywords: phosphoprotein
                                                                                                                                                                                                                                                      A;Accession: A27307
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-171 <AZE>
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C;Genetics:
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Matches 17; Conservative
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A, Molecule type: DN
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C, Genetics:

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C.Species: Homo sapiens (man)
C,Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-May-1996
C,Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-May-1996
C,Accession: D40750
G,Accession: D40750
A,Title: PRBI gene variants coding for length and null polymorphisms among human saliv A,Recession: D40750
A,Title: PRBI gene variants coding for length and null polymorphisms among human saliv A,Recession: D40750
A,Scession: D40750
A,Scession: D40750
A,Scession: D40750
A,Scession: 1-117 A&Es
A,Scession: 1-117 A&Es
A,Coss-references: GB:S62930
C,Superfamily: proline-rich protein
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C;Species: Home sapiens (man)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Aug-1997
C;Accession: B36298
R;Azen, E.A; Minaguchi, K.; Latreille, P.; Kim, H.S.
R;Azen, E.A; Minaguchi, K.; Latreille, P.; Kim, H.S.
A;Ath. J. Hum, Genet. 47, 686-697, 1990
A;Title: Alleles at the PRB3 locus coding for a disulfide-bonded human salivary prolink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dasic proline-rich peptide IB-8a - human (fragments)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dacession: D38355
R;Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Biochemistry, 30, 3351-3356, 1991
A;Title: Basic proline-rich proteins from human parotid saliva: relationships of the A;Reference number: A38355; MUID:91190884; PMID:1849422
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                                                                            Length 188;
                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                   proline-rich protein PRB1/2S (EA) - human (fragment)
                                                                            Query Match 61.5%; Score 64; DB 2; Best Local Similarity 63.2%; Pred. No. 0.65; Matches 12; Conservative 2; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 GGNKPQGPPPPGKPQGPPPQ 29
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                                                                                                                                                                                                                                      105 GNKPQGPPPGKPQGPPQQ 123
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A,Status: preliminary
A,Molecule type: protein
A,Reatuse: 1-128 «KAU»
C,Superfamily: proline-rich protein
A;Introns: 22/1; 34/1; 187/2
C;Superfamily: proline-rich protein
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Best Local Similarity
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D38355
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                                                proline-rich proteoglycan 2 precursor, parotid - rat
C;Species: Ratus norvegicus (Norway rat)
C;Abcession: B48013
R;Castle, A.M.; Castle, J.D.
R;Castle, A.M.; Castle, J.D.
A;Title: Novel secretory proline-rich proteoglycans from rat parotid. Cloning and charac
A;Reference number: A48013; MUID:93388626; PMID:8376404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dasic proline-rich peptide II-2 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: J3-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 12-Apr-1995
C;Accession: C38355
R;Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Biochemistry 30, 3351-3356, 1991
A;Title: Basic proline-rich proteins from human parotid saliva: relationships of the cov A;Reference number: A38355; MUD:91190884; PMID:1849422
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A,Accession: JH0481
A,MOLECLE type: DNA
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C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999
C;Accession: JH0481; JH0482
R;Lin, H.H.; Kousvelari, E.E.; Ann, D.K.
Gene 104, 219-226, 1991
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A; Readdues: 1-255 < CAS.
A; Readdues: 1-255 < CAS.
A; Cross-references: GB:117318; NID:g310199; PIDN:AAA03074.1; PID:g310200
C; Superfamily: proline-rich protein
C; Keywords: extracellular protein; glycoprotein; tandem repeat
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Pred. No. 0.5;
1; Mismatches 3; Indels 1
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A;Molecule type: protein
A;Residues: 1-76 < KAU>
C;Superfamily: proline-rich protein
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Best Local Similarity 72.2%
Matches 13, Conservative
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Best Local Similarity 68.8*
Matches 11; Conservative
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Residues: 1-188 <LIN>
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A, Status: preliminary
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Cispeies: Homo sapiens (man)
Cispeies: Homo sapiens (man)
Cispeies: Homo sapiens (man)
Cispeies: Or-Oct-1994 #sequence_revision 26-May-1995 #text_change 20-Aug-1999
Cispeies: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 20-Aug-1999
Cispeies: 07-Oct-1994 #sequence_revision 0.
Cispeies: 0.
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A;Status: preliminary; translation not shown
A;Status: preliminary; translation not shown
A;Status: preliminary; translation not shown
A;Acsidues: 1-38.60-112, T',114-115, P',117-121,185-271, A',273-310 <LX3>
A;Residues: 1-38.60-112, T',214-115, P',117-121,185-271, A',273-310 <LX3>
A;Cross-references: EMBL:X07882; NID:935647; PIDN:CAA30729.1; PID:9296670
B;Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O.
B;Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O.
B;Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O.
A;Title: Differential RNA splicing and post-translational cleavages in the human saliv: A;Reference number: A92492; MUD:85289325; PMID:2993301
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F;134-194/Product: basic proline-rich peptide P-F #status experimental <MAT1>.
F;196-251/Product: basic proline-rich peptide IB-4 #status experimental <MAT2>.
F;3,65,107/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: DNA
A;Residues: 35-36, EV,38-112,155-310 <LY2>
A;Cross.references: EMBL:X07704
A;Note: medium allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 GGNPQQPQAPPAGQPQGPPR 239
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C, Superfamily: proline-rich protein
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A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 35-310 <LY1>
A;Cross-references: EMBL:X07715
A;Note: large allele
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Residues: 114-194 «KAU>
.Residuental source: saliva
.Note: this peptide, which is closely related to that of peptide P-E, contains three 21
.Accession: A38355
.Molecule type: protein
.Residues: 10-67, K' «KA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Homo sapiens (man) Fig. Cispecies: Homo sapiens (man) Fig. Cispecies: Homo sapiens (man) Fig. Cispecies: ListNov-1984 #sequence revision 12-Apr-1996 #text change 08-Dec-2000 Ciscoession: E25372; A60827; A01294; B38355; A38355; F38355 R38355; R383555; R38355; R383555; R38355; R383555; R38355; R38355; R383555; R383555; R383555; R38
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; Molecule type: protein
; Residues: 134-194 cSAI>
; Experimental source: saliva
; Experimental source: saliva
; Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
; Auffman, D. Sasi-13366, 1991
; Title: Basic proline-rich proteins from human parotid saliva: relationships of the cov
; Reference number: A38355; MUID:91190884; PMID:1849422
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;Molecule type: mRMy
;Mosidues: 175-251 cMAM
;Saitoh, E.; Isemura, S.; Sanada, K.
. Biochem. 93, 883-888, 1988
. Titchem. 93, 883-888, 1983
. Titchem. 93, 883-888, 1983
;Mittle: Complete amino acid sequence of a basic proline-rich peptide, P-F, from human
;Reference number: A03294; MUID:83265674; PMID:6874669
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Residues: 1-21 cMAB>

Residues: 1-21 cMAB>

;Residues: 1-251 cMAB>

;Manula bernices: 1-251 cMAB>

;Manula, P.W.; Morley, D.J.; Larsen, S.H.; Karn, R.C.

!lochem. Genet. 26, 165-175, 1988

'Title: Expression of human salivary protein genes.

;Recession: A60827; MUID:88240287; PMID:3288192
                                                                                                                 A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.6%; Score 62; DB 2; Length 212; Best Local Similarity 57.9%; Pred. No. 1.2; Matches 11; Conservative 3; Mismatches 1; Indele
            A; Reference number: A36298; MUID:91022705; PMID:2171329
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                                                                                                                                                                                                                                                                                                                                                     A,Gene: GDB:PRB3
A,Cross-references: GDB:119513; OMIM:168840
A;Map position: 12p13.2-12p13.2
C,Superfamily: proline-rich protein
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                                                                           Accession: B36298
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C;Keywords: duplication; parotid gland; saliva; tandem repeat P;1-13/Domain: signal sequence #status predicted <SIG> F;14-206/Product: acidic proline-rich protein #status predicted <MAT> F;80-189/Region: 18-residue repeats
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Best Local Similarity 64.7%;
Matches 11; Conservative
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Tattus norvegicus (Norway rat)
C;Date: 17.Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C;Accession: A03296
R;Ziemer, M.A.; Swain, W.F.; Rutter, W.J.; Clements, S.; Ann, D.K.; Carlson, D.M.
J Biol. Chem. 259, 10475-10480, 1984
A;Title: Nucleotide sequence analysis of a proline-rich protein cDNA and peptide homolog
A;Reference number: A03296; MUID:84289443; PMID:6547951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: protein A,Residues: 54-57, E',59-73, 'R',82-101 <SHI>
R;Charlton, A.J.; Baxter, N.J.; Lilley, T.H.; Haslam, E.; McDonald, C.J.; Williamson, M. R;Charlton, A.J.; Baye-292, 1996
A,Title: Tannin interactions with a full-length human salivary proline-rich protein disp A;Reference number: S62891; MUID:96184506; PMID:8605987
                                    A; Molecule type: mRNA
A;Residues: 1-36, 'E',38-112,'T',114-115,'P',117-121,185-271,'A',273-310 <NAE>
R;Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Biochemistry 30, 3351-3356, 1991
A;Title: Basic proline-rich proteins from human parotid saliva: relationships of the cov
A;Reference number: A38355; MUD:91190884; PMID:1849422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .Shimomura, H.; Kanai, Y.; Sanada, K.
Biochem. 93, 857-863, 1983
Title: Amino acid sequences of glycopeptides obtained from basic proline-rich glycopro;
Reference number: A61294; WUID:83265671; PMID:6874667
                                                                                                                                                                                                                                                                                                                           A,Molecule type: protein
A,Residues: 241-254,'KN',257-310 <KAU>
R;Saitch, B.; Isemura, S.; Sanada, K.
Biochem. 93, 495-502, 1983
A;Title: Complete amino acid sequence of a basic proline-rich peptide, P-D, from human }
A;Reference number: A03295; MUID:83186122; PMID:6841349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 241-252 <CHA>
A;Note: amino end of peptide designated basic proline-rich protein IB-5
A;Note: it is unclear from the peptide sequence whether this is a product of the PRB2
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A)Gene: GDB:PRB4
A)Gene: GDB:PRB4
A)Gene: GDB:PRB4
A)Cross-references: GDB:119514; OMIM:180990
A)Map position: 12p13.2-12p13.2
A)Introns: 22/1; 34/1
A)Note: the list of introns may be incomplete
C)Superfamily: proline-rich protein
C)Superfamily: proline-rich poptide
C)Superfamily: proline-rich poptide
F)1-16/Domain: signal sequence #status predicted <SIG>F;1-16/Domain: proline-rich poptide P-D #status experimental <MAT>F;66.87,171/Binding site: carbohydrate (Asn) (covalent) #status predicted
F)108,150,192,213,234/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Cross-references: GB: KO2247; NID: g206395; PIDN: AAA41949.1; PID: g206396
C; Comment: This protein contains six 18- to 19-residue repeats.
C; Comment: This protein may protect teeth by binding to tannins.
C; Superfamily: proline-rich protein
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Molecule type: protein
Residues: 241-310 <SAI>
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C)Accession: A26548
R;Ann, D.K.; Gadbois, D.; Carlson, D.M.
J; Biol. Chem. 262, 3958-3953, 1987
J; Biol. Chem. 262, 3958-3953, 1987
A; Title: Structure, organization, and regulation of a hamster proline-rich protein gen A; Reference number: A26548; MUID: 87165996; PMID: 3031057
A; Accession: A26548
A; Molecule type: DNA
A; Residues: 1-183 - AANN>
A; Experimental source: parotid gland
A; Experimental source: parotid gland
C; Superfamily: proline-rich protein
F;1-14/Domain: signal sequence #status predicted <SIG>F;1-14/Domain: signal sequence #status protein H29 #status predicted <MAT>
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C;Species: Mesocricetus auxatus (golden hamster)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 15-Nov-1996
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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PRPH_MESAU
OPED_LOLEU
SYH_AERRE
PAT1_YEART
MEFD_MOUSE
SYB_LOLPE
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P70460 mus musculu P50552 homo sapien P50551 canis famil Q14684 homo sapien Q2226 mus musculu Q9uby2 homo sapien P21519 drosophila	14686 nomo sapien P32239 homo sapien Q925i9 mycobacteri O60885 homo sapien P48634 homo sapien
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ALIGNMENTS

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RECUIT 1

PREC_HUMAN

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DESCRIPT 1

PREC_HUMAN

STRANDARD, PRT, 166 AA.

DO 21-071-1966 (Rel. Ol. Created)

DT 01-071-1966 (Rel. Ol. Created)

DE 01-071-1966 (Rel. Ol. Created)

NODI-071-1966 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A frequent mutation in the acidic proline-rich protein gene, PRH2, caushing a Q147K change closely adjacent to the bacterial binding domain of the cognate salivary PRP (Prl') in Afro-Americans."; Hum. Mutat. 12:72-72(1998).

-!- FUNCTION: PRP's act as highly potent inhibitors of crystal growth of calcium phosphates. They provide a protective and reparative environment for dental enamel which is important for the integrity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schlesinger D.H., Hay D.I., "Complete primary structure of a proline-rich phosphoprotein (PRP-4), a potent inhibitor of calcium phosphate precipitation in human parotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECURICE OF 123-166 (PEPTIDE P-C).
MEDLINE=80227634; PubMed=7390979;
MEDLINE=80227634; PubMed=7390979;
MIDS and S., Satch E., Sanada K.;
MThe amino acid sequence of a salivary proline-rich peptide, P-C, and its relation to a salivary proline-rich phosphoprotein, protein C.";
MIDS and MIDS a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 17-122 (PROTEIN A).
MEDLINE-79173237; PubMed-438215;
Wong R.S.C., Hofmann T., Bennick A.;
"The complete primary structure of a proline-rich phosphoprotein from human saliva.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (In) Gross E., Meienhofer J. (eds.);
Spetides: structure and biological function (Proceedings of the 6th
American peptide symposium), pp.133-136, Pierce Chemical Co.,
Rockford II. (1979).
"The primary structure of a salivary calcium-binding proline-rich phosphoprotein (protein C), a possible precursor of a related salivary protein A."; a N."; a Biol. Chem. 255:5948(1980).
                                                                                                                                                                                                                                              human and
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Repeat; Parotid gland; Phosphorylation; Signal; Polymorphism;
Pyrrolidone carboxylic acid.
                                                                                                                                              SEQUENCE OF 17-46 (PROTEIN C).
MEDLINE-8119179; PubMed-7228490;
Schlesinger D.H., Hay D.I.;
Primary structure of the active tryptic fragments of monkey salivary anionic proline-rich proteins.";
Int. J. Pept. Protein Res. 17:34-41(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 254:4800-4808(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 17-122 (PROTEIN A).
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EMBL; K03203; AAA60184.1; -.
EMBL; M13057; AAA98807.1; -.
EMBL; M13058; AAA98808.1; -.
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Genew; HGNC:9367; PRH2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saitoh E., Isemura S., Sanada K.;
"Further fractionation of basic proline-rich peptides from human parotid saliva and complete amino acid sequence of basic proline-rich peptide P-H.";
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                HYDROXYAPATITE FORMATION, BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=85289325; PubMed=2993301;
Maeda N., Kim H.-S., Azen E.A., Smithies O.;
"Differential RNA splicing and post-translational cleavages in the human salivary proline-rich protein gene system.";
J. Biol. Chem. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINB-86243355; PubMed=3521730;

Kauffman D., Hofmann T., Bennick A., Keller P.;

Basic proline-rich proteins from human parotid saliva: complete covalent structures of proteins IB-1 and IB-6.";

Biochemistry 25:2387-2392(1986).
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13-AUG-1987 (Rel. 05, Last sequence update)
28-FBE-2003 (Rel. 41, Last amnotation update)
28-Ivary proline-rich protein precursor (Clones CP3, CP4 and Contains: Basic peptide IB-6; Peptide P-H)
                                                                                                                                                                                                                                                                           Length 166;
                                                                              INHIBIT HYDROXYAPATITE FORMATIO TO HYDROXYAPATITE AND CALCIUM. PYRROLIDONE CARBOXYLIC ACID.
        SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2.
SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 3/4.
                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                  D -> N (in allele PRH1-4).
/FIId=VAR_00553.
D -> N (in allele PRH2-1).
/FIId=VAR_005564.
                                                                                                                                                                                          /FTId=VAR 005564.
Q -> K (in allele PRH2-3).
/FTId=VAR 005565.
                                                                                                                                                                                                                                F -> P (IN REF. 10).
A7DF62BF94E3C3EF CRC64;
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Pred. No. 9.7e-06;
; Mismatches 0;
                                                                                                                      PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                   331 AA.
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MEDLINE=84161824; PubMed=6671974;
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166 AA; 17017 MW;
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                                                                                                                                                                                                                                                                                                                                    GGHPRPPRGRPQGPPQQ 17
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Best Local Similarity 100.0
Marches 17; Conservative
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46
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166
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PRP1_HUMAN
SIGNAL
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96 AA

us-10-009-709-13.rsp

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7-residue repeats.
1-residue repeats.
1-mischanbous: There are nine basic proline-rich peptides isolated FIR, B40750; PHUBE.
Phosphorylation; Repeat, Parotid gland; Pyrrolidone carboxylic acid.
MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
MOD_RES 8 8 PHOSPHORYLATION.
REPEAT 15 35 DEDUNCTURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=86243355; PubMed=3521730; Kauffman D., Hofmann T., Bennick A., Keller P.; Kauffman D., Hofmann T., Bennick A., Keller P.; Basic proline-rich proteins from human parotid saliva: complete covalent structures of proteins IB-1 and IB-6."; Biochemistry 25:2387-2392(1986).
-i- DOMAIN: Contains 21-residue repeats, two of which have internal
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Pred. No. 0.39;
                                                                                                                                                                                                                                 20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Basic proline-rich peptide IB-1.
Homo sapiens (Human).
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1 Similarity 57.1%;
12; Conservative
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PRPP HUMAN
ID PRPP_HUMAN
                                                                                                                                                             PRP5 HUMAN P04281;
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                                                                                        RESULT 4
PRP5 HUMAN
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TISSUE-saliva;
TISSUE-saliva;
MEDINE-83007119; PubMed=7118863;
ISEMURA S., Saltoh E., Sanada K.;
"Fractionation and characterization of basic proline-rich peptides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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TISSUE-Saliva;
MEDLINE-83101329; PubMed-6924859;
Kauffman D., Wong R., Bennick A., Keller P.;
"Basic proline-rich proteins from human parotid saliva: complete
"Covalent structure of protein IB-9 and partial structure of protein
IB-6, members of a polymorphic pair.";
Biochemistry 21:6558-6562(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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-!- MISCELLANDOUS: Peptides IB-9 and P-E are the same peptide.
PIR, B40750, PHUDBG.
GO; GO:0005576; C:axtracellular; NAS.
Repeat; Parotid gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.4%; Score 68; DB 1; Length 331; Best Local Similarity 61.9%; Pred. No. 0.26; Matches 13; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.6%; Score 62; DB 1; Length 61;
larity 57.1%; Pred. No. 0.25;
Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                  PEPTIDE IB-6.
PEPTIDE P-H.
Missing (in clone CP-4).
FITIGHTAR 005561.
Missing (In clone CP-5).
FITIGHTAR 005562.
A-S (IN REF. 2 AND 3).
W, 3F481FF8EBA39751 CRC64;
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                                                                                                                                                                                                                                                             Repeat; Parotid gland; Multigene family; Signal. SIGNAL 1 16 CHAIN 214 331 PEPTIDE 1B-6.
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21-UUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homo sapiens (Human).
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                            EMBL; K03204; AAA60185.1; -.
EMBL; K03205; AAA60186.1; -.
EMBL; K03206; AAA60187.1; -.
PIR; B40750; PIHUB6.
Genew; HGNC:9337; PRBL.
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331 AA; 32596 MW;
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Matches 12; Conserv
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PRPE_HUMAN
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Length 96; 3; Indels

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                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
Salivary proline-rich protein II-1 (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93385383, PubMed-8373986,
Kauffman D.L., Keller P.J., Bennick A., Blum M.,
"Alignment of amino acid and DNA sequences of human proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
59.6%; Score 62; DB 1; Length 174;
Best Local Similarity 57.1%; Pred. No. 0.68;
Matches 12; Conservative 2; Mismatches 3; Indels
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174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               printing.";
Crit. Rev. Oral Biol. Med. 4:287-292 (1993)
Go; Oc:005576, C:extracellular; NAS.
InterPro; IPRO0637, AT hook.
PRINTS; PR00929; ATHOOK.
Repeat; Parotid gland; Multigene family.
NON TER 174 174
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13 GGNQPQGPPPPPGKPQGPPPQ 33

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89121440; PubMed=2851479;
Lyons K.M., Stein J.H., Smithies O.;
Length polymorphisms in human proline-rich protein genes generated
by intragenic unequal crossing over.";
Genetics 120:267-278 (1988).
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MEDLINE=85289325; PubMed=2993301;
Maeda N., Kim H.-S., Azen E.A., Smithies O.;
"Differential RNA splicing and post-translational cleavages in the human salivary proline-rich protein gene system.";
J. Biol. Chem. 260:11123-11130(1985).
                                   SEQUENCE FROM N.A.
MEDLINE-85289325; PubMed=2993301;
Maeda N., Kim H.-S., Azen E.A., Smithies O.;
"Differential RMs splicing and post-translational cleavages in the human salivary proline-rich protein gene system.";
J. Biol. Chem. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Parotid gland; Multigene family; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALIVARY PROLINE-RICH PROTEIN PO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 62; DB 1; Length 247; Pred. No. 0.95;
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GLYCOSYLATED PROTEIN A.
MISSING (IN REP. 2).
D -> A (IN REF. 2).
W, 6A1943E435161691 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE=83265674; PubMed=6874669;
Saitoh E., Isemura S., Sanada K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 GGNPQQPQDPPAGKPQGPP 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25108 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; K03207; AAA60188.1; -. EMBL; K07882; CAA30729.1; -. PIR; S03176; PIHUSD. Genew; HGNC:9340; PRB4.
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Best Local Similarity 57.9
Marches 11, Conservative
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247
39
177
57
218
                                                                                                                                                                            SEQUENCE FROM N.A.
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NCBI TaxID=9606;
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37
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CONFLICT
SEQUENCE
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Lyons K.M., Stein J.H., Smithies O.;
"Many protein products from a few loci: assignment of human salivary
proline-rich proteins to specific loci.";
Genetics 120:255-265(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDDINE=81186121; PubMed=6841349; Saitoh E., Isemura S., Sanada K.; Saitoh E., Isemura S., Sanada K.; Complete amino acid sequence of a basic proline-rich peptide, P-D, from human parctid sailva."; J. Biochem. 93:495-502(1993).
                                                                                                                                                                        PIOIZI; PD2813;
01.MAR-1889 (Rel. 10, Created)
10.COT-1996 (Rel. 34, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
Salivary proline-rich protein PO (Allele M) [Contains: Peptide P-D]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 0.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 PEPTIDE P-D.
23676 MW; 310APP13A44E747F CRC64;
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21-UTL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary proline-rich protein PO precursor (Allele S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 AA
                                                                                                                                                             234 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO, GO:0005576; C:extracellular; NAS. Repeat; Parotid gland; Multigene family. NON_TER
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                                                                                                                                                             PRT;
                           GGH----PRPPRGRPQGPPQQ 17
                                                 26 GGNOPORPPPPGKPQGPPPO 46
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                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                     sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=9606;
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MIM; 180990; -.
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                                                                                                                                                             PRPM_HUMAN
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PRB4 HUMAN

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MEDLINE=89121439; PubMed=3220251;
Lyons K.M., Stein J.H., Smithies O.;
"Many protein products from a few loci: assignment of human salivary proline-rich proteins to specific loci.";
Genetics 120:255-265(1988).
   sequence of a basic proline-rich peptide, P-F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIOLE2; PD2813;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary proline-rich protein PO (Allele K) [Contains: Peptide P-D]
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Saltoh B., Isemura S., Sanada K.;
"Complete amino acid sequence of a basic proline-rich peptide, P-D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL TaxID=9606;
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PIR; S03176; PIHUSD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGHPR----PPRGRPQGPPQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24641 MW;
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                                                                                                                                                                                                                                                                                                                                                    EMBL; K03208; AAA60189.1; -. PIR; E25372; PIHUPF.
                          from human parotid saliva.";
J. Biochem. 93:883-888(1983)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:9338; PRB2.
   acid
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251 AA;
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   "Complete amino
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SEQUENCE
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Best Local
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                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Parotid gland; MEDLINE=86033799; PubMed=3840480; Clements S., Mehansho H., Carlson D.M.; repetitive peptide "Novel multigene families encoding highly repetitive peptide sequences. Sequence analyses of rat and mouse proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
ACIDIC PROLINE-RICH PROTEIN PRP33.
6 X 18 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence analysis of a proline-rich protein cDNA and peptide homologies of rat and human proline-rich proteins."; J. Biol. Chem. 259:10475-10480(1984).
                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Parotid gland;
MEDLINE=64289443; PubMed=6547951;
Ziemer M.A., Swain W.F., Rutter W.J., Clements S., Ann D.K.,
Carlson D.M.;
                                                                                                                                                           Length 276;
                                                                                                                                                                                           Indels
                                                                                                         PEPTIDE P-D.
; 9F494926C979441A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 260:13471-13477(1985).
-!- FUNCTION: May protect teeth by binding to tanning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D037582CED05CE6B CRC64;
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                                                                                                                                                        59.6%; Score 62; DB 1; 57.9%; Pred. No. 1.1; iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
30-MAY-2000 (Rel. 95, Last annotation update)
Acidic proline-rich protein PRP33 precursor.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                    206 AA
             MIM; 180990; -.
GO; GO:0005576; C:extracellular; NAS.
INTE-PRO; IPR000637; AT hook.
PRINTS; PR00929; ATHOOK.
Repeat; Parotid gland; Multigene family.
NON_TER
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                                                                                                                                                                                                                     1 GGHPR----PPRGRPQGPP 15
                                                                                                          276 PF
27816 MW;
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nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                           276 AA;
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ID PRP3 RAT
AC P04474;
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                                       TISSUE=Epidermis;
MEDILIE=94151381; PubMed=8108455;
MEDILIE=94151381; PubMed=8108455;
MODILIE=94151381; PubMed=8108455;
"The molecular basis of a spectral shift in the rhodopsins of two species of graud from different photic environments.";
species of graud from different photic environments.";
-i. Roc. Lond., B, Biol. Sci. 254:233-240(1993).
-i. FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY LINKED TO CIS.RETINAL. THIS RECEPTOR IS COUPLED TO THE ACTIVATION OF PHOSPHOLIPASE.
                                                                                                                                                                            -!- SUBGELLUIAR LOCATION: Integral membrane protein.
-!- PTM: Some or all of the carboxyl-terminal Ser or Thr residues may be phosphorylated.
-!- MISCELLANEOUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMUM AT 499 NM.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Opsin subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision; Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor. NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

N-LINKED (GLCNAC. . .) (PROBABLE).

BY SIMILARITY.
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000176; Opsin.
InterPro; IPR006031, XYPPX.
Pfam; PP0016; XYPPX, 8.
Pfam; PP02162; XYPPX, 8.
PRNITS; PR00237; GPCRRIODPSN.
PROSITE; PS00237; GPCRRIODPSN.
PROSITE; PS00237; GPCRRIODPSN.
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GLN/PRO-RICH.
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HSSP; P02699; 1F88.
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                             SECUENCE FROM N.A.
 NCBI_TaxID=54069;
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SEQUENCE
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Eukaryota, Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Loliginidae; Loligo.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=8116596; Pubwed=3031057;
Ann D.K., Gabbois D., Carlson D.M.;
Ann cure, organization, and regulation of a hamster proline-rich
protein gene. A multigene family.";
J. Biol. Chem. 262:3958-3963 (1987).
                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.2%; Score 59.5; DB 1; Length 183; larity 65.0%; Pred. No. 1.4; Conservative 1; Mismatches 3; Indels
            Length 206;
                                          1; Indels
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            DB 1;
1.4;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Acidic proline-rich protein HP43A precursor.
H29.
                                                                                                                                                                      183 AA
             Score 60; DB Pred. No. 1.4; 3; Mismatches
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PIR; A26548; A26548.
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            ch 57.7%;
l Similarity 64.7%;
ll; Conservative
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es 13; Conserv
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            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R HSSP, P02699, IF88.
R InterPro; IPR000176; GPCR_Rhodpsn.
R InterPro; IPR001766; GPCR_Rhodpsn.
R InterPro; IPR001766; GPCR_Rhodpsn.
R InterPro; IPR001761; XYPPX.
)R Fam; PF00001; XYPPX.
)R Pfam; PF00162; XYPPX.
)R PRONTE; PS00237; GPCRHODOPSN.
DR PROSITE; PS00237; GPCTRIN RECEP_F1 1; 1.
DR PROSITE; PS00238; OPENTEIN_RECEP_F1 2; 1.
DR PROSITE; PS00238; OPENTEIN_RECEP_F1 3; 1.
FT TRANSMEM 34 58 1 (POTENTIAL).
FT TRANSMEM 34 58 (CYTOPLASMIC (POTENTIAL).
COMMANN 59 70 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                           TISSUE-Retina;

MEDINE-91185-91185-9158727; PubMed=1900420;

Hall M.D., Hoon M.A., Ryba N.J.P., Pottinger J.D.D., Keen J.N.,

Raibil H.R., Findlay J.B.C.;

"Molecular cloning and primary structure of squid (Loligo forbesi)

rhodopsin, a phospholipase C-directed G-protein-linked receptor.";

Plochem J. 274:35-40(1991).

-!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT

MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY

LINKED TO CIS-RETINAL. THIS RECEPTOR IS COUPLED TO THE ACTIVATION

OP PHOSPHOLIPASE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: Some or all of the carboxyl-terminal Ser or Thr residues may be phosphorylated.
-!- MISCELLANDOUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMUM AI 494 NM.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Opsin subfamily.
                                                                                                                                                                                                               Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Loliginidae; Loligo.
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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                                                                                                              01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                    452 AA.
                                                                                                                                                                                               Loligo forbesi (Northern European squid)
 415 GYPPPPQGPPPQGPPPQ 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X56788; CAA40108.1; -. PIR; S14332; S14332.
HSSP; P02699; 1F88.
                                                                                 STANDARD;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                NCBI_TaxID=6618;
                                                                                 OPSD LOLFO
P24603;
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WEDLINES 99310339; PubMed=10382966;

WEDLINES 99310339; PubMed=10382966;

Rawarabayasi Y., Hinc Y., Horikawa H., Yamazaki S., Haikawa Y.,

Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,

Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,

Takamiya M., Masuda S., Funahashi T., Tanaka T., Xudoh Y.,

A Yamazaki J., Kushida N., Oguni A., Aoki K.-I., Kubota K.,

A Yamazaki J., Nomura N., Sako Y., Kikuchi H.;

"Complete genome sequence of an aerobic hyper-thermophilic

"Complete Arrory T. ATP + L-histidine + tRNA(His) = AMP +

Gliphosphate + L-histidy-t-tRNA(His).

"C -!- SUBCELLULAR LOCATION: Cytoplasmic."

"C -!- SUBCELLULAR LOCATION: Cytoplasmic."

"C -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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PIR; B72654; B72654.
HASPP, 032422; 10260.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004154; TRNA-synt_2b.
InterPro; IPR002134; TRNA-synt_2b.
InterPro; IPR002129; HGTP_anticodon; I.
Pfam; PF03129; HGTP_anticodon; I.
Pfam; PF03129; HGTP_anticodon; I.
Pfam; PF03129; ARM-INSTAR Synt Sp; I.
PROSITE; PS50862; AA_TRNA_LIGASE_II; I.
Aminoacyl-tRNA_synthetase; Protein biosynthesis; Ligase; ATP-binding;
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                                                                                                      S-palmitoyl cysteine (By similarity)
S-palmitoyl cysteine (By similarity)
MET-RICH.
N-LINKED (GLCNAC. . .) (PROBABLE).
BY SIMILARITY.
RETINAL CHROMOPHORE (BY SIMILARITY)
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30-WAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histidyl-tRNA synthetase (BC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                            55.3%; Score 57.5; DB 1; Length 452; 64.7%; Pred. No. 5.5; ive 2; Mismatches 3; Indels 1
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422 GYPPPPQGPPPQGPPPQ 438
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es 11; Conservative
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452 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GO; GO:0000932; C:cytoplasmic mRNA processing body; IDA.
GO; GO:0000932; C:cytoplasmic mRNA processing bubunit (sensu Eu. . .; IDA.
GO; GO:00006446; P:cytomosome segregation, "MP.
GO; GO:0006446; P:regulation of translational initiation; IGI.
DOWAIN 195 200 POLY-PRO.
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MEDLINE=95373282; Pubmed=7645349;
Rodriguz-Cousino N., Libil R., Neupert W., Court D.A.;
"Identification and initial characterization of the cytosolic protein
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97128274; PubMed=8972867;

Wang X., Watt P.M., Louis E.J., Borts R.H., Hickson I.D.;

Wang X., Watt P.M., Louis E.J., Borts R.H., Hickson I.D.;

Wang X., Watt P.M., Louis E.J., Borts R.H., Hickson I.D.;

Patt: a topoisomerase II-associated protein required for faithful

chromosome transmission in Saccharomyces cerevisiae.";

Nucleic Acids Res. 24:4791-4797(1996)

-!- FUNCTION: Necessary for accurate chromosome transmission during

cell division. Interacts with topoisomerase TOP2.

-!- SUBCELLULAR LOCATION: Cycoplasmic.

-!- SIMILARITY: TO S.POMBE SPBC19G7.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Topoisomerase II-associated protein PAT1.
PAT1 OR YCR077C OR YCR77C.
Saccharomyces cereviscome (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Ballesta J.P.G., Franco L., Hoenicka J., Jimenez A., Remacha M.,
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Local Similarity 60.8%; Pred. No. 12;
les 11; Conservative 1; Mismatches 1; Indels 3
   Length 438;
                                                                            5; Indels
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.27-1992 (Rel. 22, Created)
31-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Topoisomerase II.associated protein PATI.
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Query Match

54.8%; Score 57; DB

Best Local Similarity 62.5%; Pred. No. 6.1;

Matches 10; Conservative 1; Mismatches
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6 GGRPRPPRGFRDFPPE 21
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Yeast 11:581-585(1995)
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Search completed: April 6, 2004, 16:08:02 Job time: 11.9626 secs
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Best Loca Matches

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Q16038
ID Q16038
AC Q16038;
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Q16038 homo sapien
Q08041 homo sapien
Q08051 homo sapien
Q07611 rattus norv
Q15427 macaca fasc
Q15215 homo sapien
Q04118 homo sapien
Q0599 homo sapien
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                                                                                                                                                                                                                                                                                              1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                       OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_rvirus:*
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104
1 GGHPRPPRGRPQGPPQQ 17
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_nammal:*
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sp_virus:*
sp_vertebrate:*
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Q9xw73 caenorhabdi Q9yril drosophila Q9sril drosophila Q4173 drosophila Q4174 arabidopsis Q81741 arabidopsis Q81741 saccharomyc Q82eml streptomyc Q82eml streptomyc Q82eml streptomyc Q82eml streptomyc Q82eml streptomyc Q82eml streptomyc Q82eml streptomyc Q82105 mus musculu Q6115 aureobasidi Q6188 mus musculu Q6188 mus musculu Q8184 homo sapien Q81872 homo sapien Q83853 mus musculu Q8649 homo sapien Q83245 mus musculu Q8420 mus musculu Q8420 mus musculu Q8420 mus musculu Q8420 mus musculu Q84210 caenorhabdi Q84210 caenorhabdi Q84310 caenorhabdi Q84310 caenorhabdi Q84315 organ saziv Q84315 organ saziv Q84315 organ saziv Q84315 organ saziv Q84315 organ saziv	date) rata; Euteleostomi; nidae; Homo. L., Clements L.S., salivary proline-rich 4). CRC64; Length 173; Length 173; 2; Indels 4; Gaps 1;
5 Q9XW73 5 Q9VR11 5 Q9SER4 3 Q9SER4 10 Q9LV14 11 Q9LV14 11 Q9LV14 11 Q9LV33 11 Q9LV33 11 Q9LV33 11 Q9LV38 11 Q62105 11 Q62105 4 Q8L15 11 Q68SD4 4 Q8NGQ2 11 Q68SD4 4 Q8NGQ2 11 Q8S39 4 Q9VZW2 5 Q9U3C 5 Q9U3C 10 Q8H3S 11 Q8CDB2 11 Q8CDB2	NTS 73 AA. nce updat ation updatent), Vertebr ni; Homin ni; Homin ni; Homin solung for 5565 (1984 old) 25877A7C0 0.1; 2
55.8 54.8 54.8 54.8 54.8 55.9 53.8 53.8 53.8 53.8 52.9 52.4	PRELIMINARY; 96 (TIEMBLE). (96 (TIEMBLE). (903 (TIEMBLE). (904 (TIEMBLE). (905 (TIEMBLE). (10 FROM N.A. 10 FROM N.A. 14298176; Pubmeda 14298176; Pubmeda 14298176; Pubmeda 14298176; Pubmeda 1530 (11. Acad. Sci. U. 173 AAA36502.1; 174 AAA36502.1; 175 AAA36502.1; 175 AAA36502.1; 177 AAA36502.1; 177 AAA36502.1; 178 AAA36502.1; 188 AAA36502.1; 18
7118919222222222222222222222222222222222	RESULT 1 Q15214 CQ15214 CQ15214 DT 01-NOV-19 DT 01-NOV-19 DT 01-NOV-19 DT 01-NOV-19 DE Salivary OS Homo sapi OC Eukaryota SALIVAR-8 RA AZEN E.A. RY Proceins RY Procein

297 AA.

PRT;

PRELIMINARY;

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SEQUENCE FROM N.A.
STRAIN=Spraque-Dawley, TISSUE=Parotid gland,
MEDLINE=9338626, PubMed=8376404,
Castle A.M., Castle J.D.,
Castle A.M., Castle J.D.,
Novel secretory protine-rich proteoglycans from rat parotid. Cloning and characterization by expression in AtT-20 cells.",
J. Biol. Chem. 268:20490-20496(1993).
EMBL. L17318, ARA03374.1;
PIR: 18 48013; B48013; B48013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegiuus (Rat).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                           MEDLINE=93304411; PubMed=8317492;
Azen E.A., Latreille P., Niece R.L.;
"PRBI gene variants coding for length and null polymorphisms among human salivary Ps. PmS. PmS. and Pe proline-rich proteins (PRPs).";
Am. J. Hum. Genet. 53:264-278 (1993).
EMBL; S62941; AAB27289.1; -.
PIR; D40750; D40750.
NON TER
S620ENCE 358 AA; 35050 MW; DB7F87B8D5EA759E CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                                                                                65.4%; Score 68; DB 4; Length 358; 61.9%; Pred. No. 0.21;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Proline-rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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65.4%; Score 68; DB 4; Length 338;
Best Local Similarity 61.9%; Pred. No. 0.2;
Matches 13; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC044827; AAH44827.1; -. Hypothetical protein.
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SEOUTENCE 338 AA; 33344 MW; 7F54B4E5AB002261 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
      (TrEMBLrel. 01, Created),
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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|||:
|GGNQPQGPPPPGKPQGPPQQ 192
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         01-NOV-1996 (TEMBLEEL. 01
01-NOV-1996 (TEMBLEEL. 01
01-OCT-2003 (TEMBLEEL. 25
PRBLM protein (Fragment).
PRBLM.
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TISSUE=Skin;
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Q86YA1 RESULT 3 Q86YA1

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PRB2.
Homo sapiens (Human).
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SEQUENCE
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            Lin H.H., Kousvelari E.E., Ann D.K., "Sequence and expression of the MnP4 gene encoding basic proline-rich protein in macaque salivary glands."; gene 104:219-226(1991).
                                                                                                                                           Gaps
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Azen E.A., Lyons K.M., McGonigal T., Barrett N.L., Clements L.S.,
Maeda N., Vanin E.F., Carlson D.M., Smithies O.;
"Clones from the human gene complex coding for salivary proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                 61.5%; Score 64; DB 6; Length 188;
63.2%; Pred. No. 0.38;
iive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62; DB 4; Length 93;
Pred. No. 0.36;
4; Mismatches 1; Indels
                                                                                         188 AA; 19135 MW; C8E6D0B7F4DEE504 CRC64;
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                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Salivary proline-rich protein 1 (Fragment).
Homo sapiens (Human).
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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EMBL; K02576; AAA36503.1; -.
NON TER
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MEDLINE=92009216; PubMed=1916292;
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01-JUL-1997 (TrEMBLrel. 04, Crea
01-OCT-2001 (TrEMBLrel. 18, Last
01-OCT-2003 (TrEMBLrel. 25, Last
Parctid 'o' protein (Fragment).
PRB4.
                                                                                                                                                              1 GGHPR--PPRGRPQGPPQQ 17
                                                       EMBL; M81322; AAA36905.1; -.
EMBL; M81321; AAA36904.1; -.
PIR; JH0481; JH0481.
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Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                      PRELIMINARY;
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SEQUENCE
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Q15215
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MEDLINE=89121440; PubMed=2851479;
Lyons K.M., Stein J.H., Smithies O.;
Lyons K.M., Stein J.H., Smithies O.;
Lipons K.M., Stein J.H., Smithies O.;
Intragenic unequal crossing over.";
Intragenic unequal crossing over.";
EMBL: X07881; CAA30728.1; --
PIR; S10889; S10883.
                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                    Match 59.6%; Score 62; DB 4; Length 238; Local Similarity 57.9%; Pred. No. 0.89; les 11; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.6%; Score 62; DB 4; Length 382; Best Local Similarity 55.0%; Pred. No. 1.4; Matches 11; Conservative 4; Mismatches 1; Indels
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Pred. No. 1.1;
1
238 AA; 24005 MW; 4F44E947FFF3A6C1 CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 57.9%;
Matches 11; Conservative
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RESULT 11 215218

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SEQUENCE FROM N.A.

Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,

Shaffer T., Ratcilffe A., Loretz C., Lasky S., Hood L.;

"Sequence of the mouse major histocompatibility class III region.";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

BEBL; AFIOT19; AAC62480.1;

MGI:1340031; Nafball.

SEQUENCE 2157 AA; 229072 MW; 35B21F6B7C971F40 CRC64;
                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                  56.7%; Score 59; DB 11; Length 2157; 71.4%; Pred. No. 18;
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Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
SEQUENCE 2158 AA; 229201 MW; 85A5CBDCDA84A256 CRC64;
                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Last annotation update)
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Best Local Similarity 71.4<sup>5</sup>
Matches 10; Conservative
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                                                                                                               Mus musculus (Mouse)
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Mus musculus (Mouse)
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Q7TSC1
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MEDINE=84928176; PubMed=6089212;
AZEN E.A., Lyons K.M., McGonigal T., Barrett N.L., Clements L.S.,
Maeda N., Vanin E.F., Carlson D.M., Smithies O.;
"Clones from the human gene complex coding for salivary proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61; DB 4; Length 46; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOGG64; AAHOG664.1; -.
MGD; MGI:19115467; Bat2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          950 AA; 99726 MW; E41DE9AB4A66D976 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 AA; 4592 MW; FCE1D38D8DEDC173 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to RIKEN cDNA 3110039B05 gene (Fragment).
                                                                                                                                                                                         01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
Salivary proline-rich protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins.";
Proc. Natl. Acad. Sci. U.S.A. 81:5561-5565(1984).
EMBL; K02578; AAA36505.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.7%; Scor.
57.9%; Pred. No. o....
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                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                          351 GGNPQQPQAPPAGQPQGPPR 370
  1 GGHPR----PPRGRPQGPPQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 GGNPQQPQAPPAGQPQGPP 46
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ilarity 71.4%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                     Homo sapiens (Human).
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Best Local Similarity
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxiD=10090;
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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NON TER
                                                                                                                                   015218
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Q923A9

RESULT 12

2923A9

BAT2.

Best Loca Matches

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PRT; 2157 AA.

PRELIMINARY;

Q9Z1R1

RESULT 13 Q9Z1R1

0

Gaps

. 0

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Query Match
Best Local Similarity 71.4%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGHRPPRGRPQAP 14

DD 207610

AC 007610

DT 01-NOV-1996 (TEMBLEAL) 0; Last sequence update)

DT 01-NOV-1996 (TEMBLEAL) 0; Last sequence update)

DT 01-NOV-1996 (TEMBLEAL) 0; Last sequence update)

DT 01-NOV-1996 (TEMBLEAL) 1; Last sequence update)

DT 01-NOV-1996 (TEMBLEAL) 1; Last annotation update)

DT 01-NOV-1996 (TEMBLEAL) 2; Last annotation update)

DT 01-NOV-1996 (TEMBLEAL) 2; Last sequence update)

DT 01-NOV-1996 (TEMBLEAL) 2; Last annotation update)

DT 01-NOV-1996 (TEMBLEAL) 3;

DT 01-NOV-1996 (TEMBLEAL) 3;

DT 01-NOV-1996 (TEMBLEAL) 3;

RATENDAL 2003 (TEMBLEAL) 3;

CS Rattus norvegicus (Rat)

CS Rattus (Rattus norvegicus (Ratus)

CS R
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Gaps

Ouery Match 55.8%; Score 58; DB 11; Length 170; Best Local Similarity 64.7%; Pred. No. 2.2; Matches 11; Conservative 2; Mismatches 2; Indels

Search completed: April 6, 2004, 16:14:44 Job time : 61.5629 secs

2 GHPR--PPRGRPQGPPQ 16

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6, 2004, 15:29:39; Search time 95.1682 Seconds (without alignments) 50.472 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                  - protein search, using sw model
                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                       104
1 GGHPRPPRGRPQGPPQQ 17
                                                                                                                                                                   US-10-009-709-13
                                                                                                    April
                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                          Scoring table:
                                                                    OM protein
                                                                                                                                                                                                      Sequence:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* geneseqp2000s:* geneseqp2001s:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2002s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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	uo	Human sa	Peptide	Peptide	Human bon	Human bra	Human liv	Human per	Human NOV	Human sec	Human PRH	Human sal	Human GEN	Human GEN	Human pro	P-C ge	Human Pr		Rat Prote	Human GEN	Human GEN	Human sal	Gene 13 h	Amino aci		Amino aci
	Description	Aab48783	Abb38848	Aam32323	Aam72058	Aam59494	Abg53742	Abg41873	Abr57423	Abr56769	Ada83798	Adc98216	Abp76137	Abp75971	Aaw03557	Aap93320	Add45740	Add45442	Ade57105	Abp75970	Abp76136	Aab48777	Aab34155	Aaw50193	Aa030249	Aaw50192
SUMMAKIES	ID	AAB48783	ABB38848	AAM32323	AAM72058	AAM59494	ABG53742	ABG41873	ABR57423	ABR56769	ADA83798	ADC98216	ABP76137	ABP75971	AAW03557	AAP93320	ADD45740	ADD45442	ADES7105	ABP75970	ABP76136	AAB48777	AAB34155	AAW50193	AA030249	AAW50192
	DB	4,	4	4	4	4	4	Ŋ	ω	9	ø	7	ø	9	(1	Н	7	7	7	9	φ	4	'n	N	ω	Ŋ
	Length	17	132	m	132	m	132	m	4	S	166	166	0	106	44	45	331	σ	σ	Н	н	10	49	82	117	124
æ	강당	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100,0	67.3	67.3	66.3	66.3	65.4	63.8	63.9	61.5	61.5	6	59.6	59.6	59.6	59.6
		104	104	104	104	104	104	1.04	104	104	104	104	70	70	69	69	68	66.5	66.5	64	64	62	62	62	62	62
	sult No.	1 1	7	m	4	w	v	7	œ	σv	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aao30407 Human sec	Aao30246 Human Sap	Aao30188 Human cP3	Abull891 Human ABC	Aao30408 Human sec	Abg15767 Novel hum		Aaw03556 Octadecap	ເດ	Aao00989 Human pol		Abp76681 Streptomy	Abb58372 Drosophil	Aab34161 Gene 17 h	Abb61702 Drosophil	Aag26069 Zea mays	Abr53413 Protein s	Aab48778 Human sal	Aao30248 Human Sap	Aay65869 Germline	
AAO30407	AA030246	AA030188	ABU11891	AA030408	ABG15767	ABG18110	AAW03556	AAG22606	AA000989	AAB48776	ABP76681	ABB58372	AAB34161	ABB61702	AAG26069	ABR53413	AAB48778	AAO30248	AAY65869	
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162	192	208	247	267	591	591	18	158	125	10	19938	82	91	315	106	196	6	41	64	
59.6	59.6	59.6	59.6	59.6	59.6	59.6	58.7	57.2	56.7	55.8	55.8	54.8	4	4	4	54.3	53,8	53.8	53.8	
62	62	62		62	62	62	61				80		57	57	v		Ŋ	98	99	
			6			32	<u>ო</u>	34	35	36	37			40		42	43	44	45	

ALIGNMENTS

RESULT 1

Human; PRP-1; proline-rich protein; saliva; dental caries; chromosome 12p13.2; arginine catabolism; ammonia production; pH increase; oral bacterium; caries prevention. Human saliva PRP-1 fragment (residues 99-115), SEQ ID NO:13. AAB48783 standard; peptide; 17 AA 17-MAY-1999; 99SE-00001773. 11-MAY-2000; 2000WO-SE000930. Stroemberg N, Johansson I; (first entry) (STRO/) STROEMBERG N. (JOHA/) JOHANSSON I. WO200069890-A1. Homo sapiens. 09-MAR-2001 23-NOV-2000. AAB48783; AAB48783

WPI; 2001-031923/04.

New oligopeptides comprising 2 arginine residues from degradation of proline-rich proteins, useful for preventing dental caries.

Claim 2; Page 24; 36pp; English.

The invention relates to human PRP-1-derived oligopeptides (AAB48771-AAB48783) which contain at least two arginine residues and which protect against dental caries. PRBs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are potential determinants of a person's susceptibility to dental caries. PRPs are degraded by Actinomyces and Streptococcus species to small peptide fragments. These are metabolised by oral bacteria for mutritional purposes, with certain bacterial species generating ammonia via the catabolism of arginine. The peptides of the invention, being arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby protecting the teeth against caries. Sequences AAB48771-B48783 represent the PRP-1-

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying sene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                       Peptide #6360 encoded by probe for measuring placental gene expression.
                                                                                                                                                       microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 32592; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank
                          AAM32323 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM72058 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGHPRPPRGRPQGPPQQ 97
                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGHPRPPRGRPQGPPQQ 17
                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488897/53.
                                                                                                                                                                        genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 132 AA;
                                                                                                                                                                                                                                     WO200157272-A2
                                                                                        17-0CT-2001
                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001
                                                         AAM32323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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        AAM32323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ffp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                             Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                             Peptide #6354 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 31483; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 104; DB 4; Length 132; 100.0%; Pred. No. 4:1e-05; ive 0; Mismatches 0; Indels
                                                                     17;
                                                                                                   Indels
                                                                       Length
                                                              100.0%; Score 104; DB 4;
100.0%; Pred. No. 6.6e-06;
ive 0; Mismatches 0;
derived oligopeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
                                                                                                                                                                                                                                              ABB38848 standard; peptide; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                        GGHPRPPRGRPQGPPQQ 17
                                                                                                                                1 GGHPRPPRGRPQGPPQQ 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0207456P.
2000US-00608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0180312P
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                                                                                                                                                                                                                                                                                                              (first entry)
                                                                              Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 132 AA;
                                 Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001
                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                 Best Loc
Matches
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ABB38848
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0
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                  Human bone marrow expressed probe encoded protein SEQ ID NO: 32364.
                                                                .
0
                         Length 132;
                                                             Indels
100.0%; Score 104; DB 4; 1
100.0%; Pred. No. 4.1e-05; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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RESULT 3

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us-10-009-709-13.rag

Tue Apr

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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver.
                                                                           Single exon nucleic acid probes for analyzing gene expression in human. brains.
                                                                                                                                                                        present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
                                                                                                                                 Example 4; SEQ ID NO 31599; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                     Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 104; DB 4;
100.0%; Pred. No. 4.1e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 32390; 658pp; English.
    띪
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human liver peptide, SEQ ID No 32390.
    Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene expression in human adult liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG53742 standard; peptide; 132 AA.
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    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGHPRPPRGRPQGPPQQ 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312P.
26-WAY-2000; 2000US-0207456F.
30-UWN-2000; 2000US-00608408
03-AUG-2000; 2000US-0652366.
21-SEP-2000; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2000; 2000US-0236359P, 04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                      the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 GGHPRPPRGRPQGPPQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 100.
Matches 17; Conservative
Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG, Hanzel DK,
                                      WPI; 2001-483446/52
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                                                                                                                                                                                                                                                                                                                              Sequence 132 AA;
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  Penn SG,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human brain expressed single exon probe encoded protein SEQ ID NO: 31599.
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100.0%; Pred. No. 4.1e-05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                    Rank DR;
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100.08;
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                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                         30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGHPRPPRGRPQGPPQQ 17
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                                                30-JAN-2001; 2001WO-US000668
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2000US-00608408.
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27-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                        WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157275-A2.
                                                                                     04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-2001
              09-AUG-2001
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Matches
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(I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at Etp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human peptide encoded by genome-derived single exon probe SEQ ID 31538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial dispathic pulmonary fibrosis; neurofibromatosis; tubercous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histlocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary dyskinesis; pulmonary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                 Query Match 100.0%; Score 104; DB 4; Length 132; Best Local Similarity 100.0%; Pred. No. 4.1e-05; Matches 17; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                measure gene expression in human lung samples.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-114183/15
                                                                                                                                                                                                Seguence 132 AA;
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ABG41873
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probes. Also included are a microarray comprising the novel set of probes which hybridies at high stringency to a nucleic acid expressed in the human lung; measuring sene expression in a sample condidexived from human lung; measuring sene expression in a sample collection of detectably labeled mucleic acids derived from human lung measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in eukaryotic genome, comprising (a) array; dentifying exons in eukaryotic genome, comprising (a) the eukaryotic; and (b) detecting specific hybridisation of detectably the eukaryotic; and (b) detecting specific hybridisation of detectably collabeled nucleic acids from eukaryote lung mRNA, to a single exon probe, the rangement identical to the predicted exon, the probe is included in the above amed incorarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in the expression of the exons in the tissues and/or cell types using hybridisation to a single exon microarray having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene, a peptide comprising one of probes/open reading frames (ORF). The probes are used for gene expression of the exons in the tissues and/or encoded by the probes/open reading frames (ORF). The probes are used for gene expression clustering the mans of the exons in a gene, particularly using human clung desames (ILD), familial idopathic pulmonary fibrosis, pulmonary interstitial lung disease (ILD), familial idopathic pulmonary disease (OCDD), interstitial lung derived mRNA syndrome, fibrocystic pulmonary disease (OCDD), interstitial lung derived manalysis, pulmonary hypertensis, pulmonary hypertensis, pulmonary hypertensis, pulmonary hypertensis, pulmonary hypertension and hyaline membrane disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 4.1e-05;
tive 0; Mismatches 0; Indels
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ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABR57412 to ABR57435. (I) have cytostatic, cardiant, antiinflammatory, nootropic, immunosuppressive, antiallargic, haemostatic, antibacterial, viruoide, antiartritic, hepatotropic, antiasthmatic, nephrotropic, viruoide, antiparasitic, anticonvulsant, hypotensive, vasotropic, antiparasitic, anticonvulsant, hypotensive, vasotropic, antiparkinsonian, antiparasitic, anticonvulsant, hypotensive, vasotropic, antiparkinsonian, cynlogenic and antianglogenic activities, and can be used in gene therapy and vaccines. The NOVX polypeptides and their antibodies can be used to determine the presence or absence of (I) in a sample. The NOVX polypeptides, polymoral and antiabodies and antibodies against them, are useful in manufacturing a medicament for treating or preventing a syndrome associated with a NOVX-associated disorder such as hypertension, autoimmune disorders, allergies, blood disorders asthma, inflammation, autoimmune disorders, allergies, blood disorders, obesity, acquired immunodeficiency syndrome (ADS), immunoglobulin (19)A nephropathy, cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goire, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystropity, epilepsy, and other wasting disorders associated with chronic diseases. ACF03571 to ACF03544 represent PCR primers and probes for NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New NOVX polypeptide useful for preventing or treating NoVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                                                                                                                                                                           M, Macdougall JR, Smithson G, Millet I, Stone DJ;
E, Ellerman K, Alsobrook JP, Lepley DM, Burgess CE;
CA, Edinger SR, Gangolli EA, Gorman L, Taupier RJ, Li L;
Fernandes ER, Vernet CAM, Tchernev VT, Casman SJ, Shenoy
', Furtak K, Baumgartner JC, Colman SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 69; 346pp; English.
                                            02-NOV-2000; 2000US-0245291P.
02-NOV-2000; 2000US-02451JTP.
07-NOV-2000; 2000US-024662P.
08-NOV-2000; 2000US-0246871P.
26-JAN-2001; 2001US-0264389P.
26-JAN-2001; 2001US-0264439P.
29-JAN-2001; 2001US-0264439P.
02-NOV-2001; 2001WO-US051580
                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP
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N-PSDB; ACF03558.
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                                                                                                                                                                                                                                                                             Grosse WM,
Gunther E,
Spytek KA,
Guo X, Fern
Mishra V, F
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Gaps ö Score 104; DB 6; Length 149; Pred. No. 4.5e-05; 0; Mismatches 0; Indels (100.08; Query Match
Best Local Similarity 100.

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98 GGHPRPPRGRPQGPPQQ 114 GGHPRPPRGRPQGPPQQ 17

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ABR56769 standard; protein; 154 AA. 30-JUL-2003 (first entry) ABR56769; RESULT

Human secreted protein SECP-44 SEQ ID NO:44.

Human; secreted protein; SECP; cytostatic; antiarteriosclerotic; antionvoltsant; noctropic, neuroprotective; cerebroprotective; anti-HIV, antiallergic; antiinflammatory; thyromimetic; gene therapy; cancer; cell proliferative disorder; atherosclerosis; neurological disorder;

epilepsy; Huntington's disease; stroke; immune disorder; allergy; AIDS; inflammatory disorder; developmental disorder; hypothyroidism; Cushing's syndrome; infection. H Lal PG, Yue H, Honchell CD, Baughn MR, Duggan BM, Tran UK, TW, Lee S, Thangavelu K, Yue H Tang TY, Warren BA, Gietzen KJ, Lal PG, Yue H, Honchell CD;
Lehr-Mason PM, Burford N, Xu Y, Baughn MR, Duggan BM, Tran UK;
Lee EA, Forsythe IJ, Richardson TW, Lee S, Thangavelu K, Yue F
Emerling BM, Walla NK, Azimzai Y, Sanjanwala B, Hafalia AJA;
Borowsky ML, Nguyen DB, Ison CH, Astromoff A, Ding L, Lee SY;
Becha SD, Ramkumar J, Gandhi AR, Jin P, Fu GK, Swarnakar A; 17-AUG-2001; 2001US-0313249P.
24-AUG-2001; 2001US-0314752P.
07-SEP-2001; 2001US-0317824P.
07-SEP-2001; 2001US-0317824P.
21-SEP-2001; 2001US-032464P.
24-SEP-2001; 2001US-032486P.
02-NOV-2001; 2001US-034328P.
13-FEE-2002; 2002US-035202P. 19-MAR-2002; 2002US-0366041P. 30-APR-2002; 2002US-037698BP. 15-AUG-2002; 2002WO-US027143 (INCY-) INCYTE GENOMICS INC. WPI; 2003-278569/27. N-PSDB; ACC79069 WO2003016506-A2 Homo sapiens. 27-FEB-2003

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and New human secreted proteins (SECP), useful for diagnosing, treating preventing diseases or conditions associated with the aberrant SECP expression e.g. cancer, AIDS, atherosclerosis, Huntington's disease, stroke, infections.

Claim 1, Page 222, 286pp, English.

ACT 9026 to ACC79105 encode the human secreted proteins (I) given in ABR56726 to ABR56805, designated SECP-1 to SECP-80. SECP sequences can harderic, antilaterioxuvlsant, antilatiflammaacory, nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic and thyromimetic activities, and can be used in deme therapy. The SECP proteins and polymucleotides can be used in diagnosancy, treating and preventing diseases or conditions associated with the decreased concer, atherosclerosis), neurological (e.g. epilepsy, Huntington's cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, Stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of SECP. The SECP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that expression of the target polymucleotide and compounds that expression of contract the activity of the polypeptide

Sequence 154 AA;

Gaps ö Length 154; Indels 100.0%; Score 104; DB 6; 100.0%; Pred. No. 4.7e-05; tive 0; Mismatches 0; Local Similarity 100. ses 17; Conservative Query Match Best Loc Matches

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ò 셤 ADC98216 standard; protein; 166 AA.

ADC98216;

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expressed sequence tag; EST; arabidopsis; tumour; phenotype; hyperosmotic stress; colon cancer; immunogen;
                                                                                                                                                                                                                                                                                                 Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
                                                                                                                                                                                                                                                       Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
                                                                                                                                                                                                                                                                                                                                            Claim 29; Page 191-192; 516pp; English.
                ADA83798 standard; protein; 166 AA.
                                                                                                                                                                                30-MAY-2002; 2002WO-IB004189.
                                                                                                                                                                                                30-MAY-2001; 2001US-0293999P.
22-OCT-2001; 2001US-0330457P.
19-FEB-2002; 2002US-0357144P.
                                                  20-NOV-2003 (first entry)
                                                                                                                                                                                                                                     (BIOM-) BIOMEDICAL CENT
                                                                                                                                                                                                                                                                        2003-175241/17.
                                                                     Human PRH2 protein
                                                                                                                                                                                                                                                                        WPI; 2003-175241/
N-PSDB; ADA83797.
                                                                                                                                             WO2002103028-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 166 AA;
                                                                                        human; marker;
stress-induced
                                                                                                                          Homo sapiens.
                                                                                                                                                              27-DEC-2002
                                  ADA83798;
                                                                                                         vaccine.
RESULT 10
```

The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTS) known to be expressed in the phenotype/cell type of interest with all ESTS expressed in normal tissue phenotype/cell type of interest with all ESTS expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably arbidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method as a tumour cell, and the predetermining the progression of colon or free invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell. An antibody of the invention is useful for detecting the absence or presence of peptides encoded by tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a tumour-associated antigen of the invention.

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Gaps

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100.0%; Score 104; DB 7; 100.0%; Pred. No. 5e-05; iive 0; Mismatches 0

Query Match
Best Local Similarity 100.
Matches 17; Conservative

7; Length 166; Indels

> Gaps ö 100.0%; Score 104; DB 6; Length 166; 100.0%; Pred. No. Se-05; 1.ve 0; Mismatches 0; Indels C Query Match
> Best Local Similarity 100.0

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ABP76137 standard; protein; 106 AA.

(first entry)

21~FEB-2003

ABP76137;

RESULT 12
ABP76137
ID ABP76
XX
AC ABP76
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DT 21-FE
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RESULT 11 ADC98216

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The invention relates to the human atopic dermatitis-inducing proteins, salivary acidic proline-rich phosphoprotein (PRP; ADC98216) and prolactin cinducible protein (PIP; ADC98218), and their post-translationally modified forms. These proteins are secreted by salivary or sweat glands and bind to IgB autoantibodies, thereby activating mast cells and sasophils. The invention also relates to antigenic peptide fragments of RPP or PIP; antibodies which bind to PRP or PIP; methods for diagnosing atopic dermatitis or for determining whether an individual is at risk of developing atopic dermatitis by determining the presence of PRP- or PIP-specific antibodies or immune complexes, or by quantifying histamine release; and sensitisation remedies for atopic dermatitis containing PRP antibodies are useful in diagnosing atopic dermatitis, or for determining whether an individual is at risk of developing atopic dermatitis. They are also useful in diagnosing atopic dermatitis. They are also useful in developing sensitisation remedies for the treatment of atopic dermatitis. The present sequence represents the specifically claimed human salivary acidic proline-rich phosphoprotein (PPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atopic dermatitis-inducing proteins, applicable in diagnosis of including risk of onset, and in developing sensitization remedies for the disease.
                                                                                                                                                           Human, salivary acidic proline-rich phosphoprotein, PRP, autoantigen, aropic dermatitis-inducing protein, salivary gland, igs autoantibody; immunoglobulin E; mast cell activation; basophil activation; diagnosis; risk aggessment; sensitisation remedy; dermatological; antiallergic;
                                                                                                                     Human salivary acidic proline-rich phosphoprotein (PRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Koro O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 2; 43pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tanaka T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NISC-) JAPAN SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-2003; 2003WO-JP004325
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-2002; 2002JP-00105425
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hide M, Yamamoto S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-833567/77.
                                                                                                                                                                                                                                           antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADC98215
                                                                                                                                                                                                                                                                                                                            WO2003084991-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 166 AA;
                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                              01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2003
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Human GENSET protein SEQ ID 463

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The present invention relates to novel GENSET polynuclectides (AB236404-
BA25621) encoding polypeptides (AB975963-ABP76368). The polynucleotides
and polypeptides are useful in screening and diagnostic assays for
abnormal GENSET expression and/or biological activity. They are also
useful for screening of compounds for treating or preventing GENSET-
related disorders, such as heavy metal toxicity, cancer, inflammatory
diseases, immune disorders, and the neuromuscular, central nervous system
(CNS), cardiovascular or gastrointestinal effects of the toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                         Cytostatic, antiinflammatory, nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GBNSET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 70; DB 6; Length 106;
Pred. No. 0.37;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards J, Jobert S,
                                                                                                                                                              central nervous system; cardiovascular; gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 537; 735pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP75971 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2001; 2001WO-IB000914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-2001; 2001WO-IB000914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-2001; 2001WO-IB000914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.3%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ||:|:|||||||
PPPPQGKPQGPPQQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PRPPRGRPQGPPQQ 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanaka H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-075548/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 106 AA;
                                                                                                                                                                                                                                                                                   WO200283898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200283898-A1.
                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bejanin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ3691) encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the sequence of the human proline-rich saliva glycoprotein P-C which was used to synthesise an octadecapeptide (AAW03556) which has an insulin secretion promoting activity and a glucagon secretion inhibiting activity. The peptide was generated by usual peptide synthesis method and opt. contains Boc protective gps. at the N-terminal His and on the residue during synthesis. These are removed by cleavage with HCl for 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; saliva; proline-rich glycoprotein; insulin; secretion; glucagon; perfusion pancreas model; Wistar rat; diabetes
                                                                                                                               New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and tneuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New octadeca:peptide for treating diabetes - acts as insulin secretion promoter and glucagon secretion inhibitor.
                                                                   Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB 6; Length 106;
Pred. No. 0.37;
                                                                   Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                 Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human proline-rich saliva glycoprotein P-C.
                                                                                                                                                                                                                  Claim 14; Page 404-405; 735pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TEIK ) TEIKOKU HORMONE MFG CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW03557 standard; peptide; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 2; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%;
78.6%;
18-APR-2001; 2001WO-IB000914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PRPPRGRPQGPPQQ 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.3
Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 PPPPGGKPQGPPQQ
                                                                 Tanaka H,
                                                                                                 WPI; 2003-075548/07
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 106 AA;
                              (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; saliva;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                               Bejanin S,
                                                                                                                                                                                  toxicity
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Gaps .; 0

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Giordano J;

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mins on ice. The insulin secretion promoting activity and glucagon secretion inhibiting activity were measured in a perfusion pancreas model in a male Wister rat. Insulin secretion was 1.78 times than normal and glucagon secretion was 0.77 times normal levels. The peptide can thus be used to treat diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DNA encoding it is prepd. as 14 oligomers. The 5' terminal of 12 of the oligomers is phosphorylated, complementary 2 or 3 oligomers are annealed, and the resulting 6 ds DNAs are combined to form the P-C gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purificn. of fused protein(s) - comprises contacting fused protein with silica gel absorbent and eluting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Gaps
                                                                                                                                                         Gaps
                                                                                                                                                           4.
                                                                                                                       Query Match 66.3%; Score 69; DB 2; Length 44; Best Local Similarity 61.9%; Pred. No. 0.22; Matches 13; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.3%; Score 69, DB 1; Length 45, Best Local Similarity 61.9%; Pred. No. 0.23; Matches 13; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    P-C gene; fused protein; silica gel absorbent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 GGHQQGPPPPPGKPQGPPPQ 31
                                                                                                                                                                                     1 GGH----PRPPRGRPQGPPQQ 17
                                                                                                                                                                                                        10 GGHQQGPPPPPGKPQGPPPQ 30
                                                                                                                                                                                                                                                                                             AAP93320 standard; protein; 45 AA.
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                                                                                                                                                                                                                                                                                                                                                        19-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TORA ) TORAY IND INC.
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N-PSDB; AAN92373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45 AA;
                                                                                              Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-1987;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Search time 66.729 Seconds (without alignments) 66.909 Million cell updates/sec

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

	Application	, , , , , , , , , , , , , , , , , , , ,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Segmence 43644 B	Semience 80 Anni	Sequence 7. Appli	Segmence 1418 An	Semience 12127 A	Sequence 61067. A	Sequence 5. Annli	Semience 66. Anni	Sequence 21. Appl	Sequence 259584.	Seguence 171613	Section 68908	Semience 40613. A	Semience 39176. A	
, QI	US-09-864-761-43644	US-10-157-031-80	US-10-084-846A-7	US-10-374-780A-1418	US-10-156-761-12127	US-10-425-114-61067	US-10-084-846A-5	US-09-888-615-66	US-10-311-035-21	US-10-424-599-259584	US-10-424-599-171613	US-10-425-114-68908	US-10-425-114-40613	US-10-425-114-39176	US-10-424-599-277859
DB		14	15	13	14	12	15	σ	16	12	12	12	12	12	12
% Query Match Length DB	132	166	19652	191	310	398	19723	953	953	123	149	240	299	539	52
% Query Match	100.0	100.0	55.8	53.8	53.8	53.8	53.8	53.4	53.4	52.9	52.9	52.9	52.9	52.9	52.4
Score	104	104	58	99	99	56	56	55.5	55.5	55	22	55	55	55	54.5
Result No.	1	7	m	4,	S	9	7	ω	σ	10	11	12	13	14	15

o,	1716	21918	38, A	e 206	e 2. A	Sequence 1002, Ap	e 1002	280	185	892	equence 278	equence	equence 6,	equence 701	equence 1109, A	equence 1	equence 1	equence 1	N	equence 2	equence 2	equence 2	~	equence 1	equence 6	equence 3	equence 2	9	o)
2 US-10-424-599-17739	2 US-10-424-599-1	2 US-10-424-599-21918	US-08-424-550B-	2 US-10-424-599-2	0 US-09-959-987	US-09-925-299-100	0 US-09-925-299-1	1 US-09-833-245-28	2 US-10-424-599-18	1 US-09-764-875-89	0 US-09-919-039-27	2 US-10-114-270-8	5 US-10-084-846A-	2 US-10-425-114-701	0 US-09-933-767-110	US-10-023-28	US-10-424-599-1485	4-599-189	US-10-424-599-285	US-10-424-599-	US-10-424-599-2334	US-10-127-940-	US-10-441-757-	US-09-443-745-1	US-10-222-772-6	US-10-369-493-34	US-10-200-56	US-10-237-551-20	US-10-237-551-25
	55 1	62 1	45	69 1	41 1	47	47 1	07 1	31 1	51 1	07 1	17 1	662 1	65 1	-	-	7	-	-	95 1	7	51 1	51 1	52 1	008 1	028 1	22 1	122 1	122 1
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16	17	18	13	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	4.2	43	44	45

ALIGNMENTS

APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
APPLICANT: Chan, Wensheng
TITLE OF INVENTION: HUMBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOF
TITLE OF INVENTION: HUMBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION HUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,366
PRIOR FILING DATE: 2000-00-03
PRIOR PRIOR FILING DATE: 2000-00-03
PRIOR PLICATION NUMBER: PCT/USO1/0066
PRIOR APPLICATION NUMBER: PCT/USO1/0066
PRIOR APPLICATION NUMBER: PCT/USO1/0066
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30 Sequence 43644, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:

¹ GGHPRPPRGRPQGPPQQ 17 US-10-009-709-13 Perfect score: Sequence:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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) OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 2.; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
US-10-084-846A-7
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APPLICANT: Reuber, T. Lynne
APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Percel
APPLICANT: Procedie, James
APPLICANT: Pilgrim, Marsha L
APPLICANT: Pubell III, Arnold T
APPLICANTON NUMBER: US/37,94
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICANION NUMBER: 06/336,692
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2002-06-09
PRIOR FILING DATE: 2002-06-09
PRIOR FILING DATE: 2002-06-09
PRIOR FILING DATE: 2002-06-09
PRIOR PRIOR FILING DATE: 2002-06-09
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                                                                                                                   APPLICANT: WEITHAUBE, GABRIELE
APPLICANT: WHILENWEG, AGNES
APPLICANT: WHILENWEG, AGNES
APPLICANT: WHERENE, AXEL
APPLICANT: HEREZER, AXEL
APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REPERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PATCHIN VOY: 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Streptomyces viridochromogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sherman, Bradley K
APPLICANY: Riechmann, Jose Luis
APPLICANY: Jiang, Cai-Zhong
APPLICANY: Heard, Jacqueline E
APPLICANY: Haake, Volker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Creelman, Robert A
Ratcliffe, Oliver
Adam, Luc J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2258 GTPRPPRGRGRGP 2270
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| Publication No. US20030108890A1
| Publication No. US20030108890A1
| Publication No. US20030108890A1
| APPLICANT: Baranova, A. V. |
| APPLICANT: Kolovakaya, N. K. |
| APPLICANT: Kolovakaya, L. L. |
| APPLICANT: Krukovskaya, L. L. |
| APPLICANT: Krukovskaya, L. L. |
| APPLICANT: Krukovskaya, L. L. |
| TILL OF INVENTION: In silico screening for phenotype-associated expressed sequences |
| FILE REPRENCE: 2760-103 |
| CURRENT APPLICATION NUMBER: US/10/157,031 |
| CURRENT PILING DATE: 2002-05-30 |
| NUMBER OF SEQ ID NOS: 415 |
| SOOTWARE: Patentin version 3.1 |
| SEQ ID NO 80 |
| LENGTH: 166 |
| LENGTH: 166 |
| OFFICE O
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN UDNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BEARENS, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.0
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: SYPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: SYPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: SYNESPROT HIT: PRO2010, EVALUE 7.40e-02
US-09-864-761-43644
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100.0%; Score 104; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 17; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 104; DB 9; Length 132;
Best Local Similarity 100.0%; Pred, No. 0.00033;
Matches 17; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00670
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR PELICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
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US-10-157-031-80
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US-10-084-846A-7
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ò g ; Sequence 7, Application US/10084846A

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OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1. OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
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                                                                                                                                                                                                                                                                            Ouery Match 53.8%; Score 56; DB 12; Length 398; Best Local Similarity 66.7%; Pred. No. 1.3e+02; Matches 10; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: LIB3279-185-B11_FLI.pep
US-10-425-114-61067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-084-946A-5

Sequence 5, Application US/10084846A

Sequence 5, Application US/10084846A

Publication No. US20040006026A1

SERENAL INFORMATION:
APPLICANT: WELTNAUER, GABRIELE
APPLICANT: WHLENWEG, AGNES
APPLICANT: TREFEZE, AXEL
APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A

CURRENT FILING DATE: 2003-02-25
FRIOR FILING DATE: 2001-08-24
FRIOR FILING DATE: 2001-08-24
FRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120

SOFFWARE: Patentin Ver. 3.2

LENGTH: 19723
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APPLICANT: PLOWMAN, GREGORY
APPLICANT: CHANTON:
APPLICANT: CHANTON:
APPLICANT: CHANTON:
APPLICANT: CHANTON:
APPLICANT: CHANTON:
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVEXTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DAFE: 2001-06-26
FRICH APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10177 GGHRTSGRRPRGRPRGPGQ 10196
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Patent No. US20020064856A1
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  CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 61067
                                                                                                                                                                                                                                                                                                                                                                                                                                            196 GHEPRAPLGRPODPP 210
                                                                                                                                                                                                                                                                                                                                                                                       1 GGHPRPPRGRPQGPP 15
                                                                                                           TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-084-846A-5
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                                                                                      LENGTH:
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Publication No. US20040034888A1
Publication No. US20040034888A1
SEQUENCE INFORMATION
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Sovalic, David K.
APPLICANT: Sovalic, David K.
APPLICANT: Go, Yongwei
APPLICANT: Tabaska, Jack E
APPLICANT: VIOLET Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                            Query Match 53.8%; Score 56; DB 15; Length 191; Best Local Similarity 57.1%; Pred. No. 68; Matches 12; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMER, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIRAM, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI WOSHIYKI
ITILE OF INVENTION: NOVEL POLINUCLEOTIDES
FILE REPERENCE: 299-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
SRO ID NO 12227
LENGTH: 310
                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Orthologous to G1073
US-10-374-780A-1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12127, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION WUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: Patentin version 3.2
SEQ ID NO 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptomyces avermitilis US-10-156-761-12127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGHPRPPRGRPQG-----PP 15
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Best Local Similarity 66.7*
                                                                                                                                                                                                                         ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-10-156-761-12127
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US-10-425-114-61067
                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                       FEATURE:
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Gaps

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RESULT 11

US-10-444-599-171613

Sequence 17 No. US20040031072A1

SEQUENCE 17 No. USANTION:

SEQUENCE 18 No. USANTION:

SEQUENCE 18 No. USANTION:

SEQUENCE 18 No. USANTION:

SEQUENCE 18 NO. USBN 18 NO.
                                                                                                                                                              Sequence 255584, Application US/10424599

Fublication No. US20040031072A1

GENTRAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Coro Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILLE REPERRENCE: 38-010-01424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

SEQ ID NO 259584

LENGTH: 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.9%; Score 55; DB 12; Length 149; llarity 58.8%; Pred. No. 70; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_125982C.1.pep
US-10-424-599-171613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7642C.1.pep
US-10-424-599-259584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (1)..(123)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-425-114-68908
; Sequence 68908, Application US/10425114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 GKRDTPKRGRÞGGPÞÓK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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TITLE OF INVENTION: Proteases
FILE OF DEPOSE FILE OF OUR PROSEST OF SET OF OUR PROSEST OF SET OF OUR PROSEST OF SET OF SET OF OUR PROSEST OF SET OF 
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53.4%; Score 55.5; DB 16; Length 953;
Best Local Similarity 57.9%; Pred. No. 3e+02;
Matches 11; Conservative 1; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.4%; Score 55.5; DB 9; Length 953; Best Local Similarity 57.9%; Pred. No. 3e+02; Matches 11; Conservative 1; Mismatches 4; Indels
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; CTHER INFORMATION: Incyte ID No. US20040023243A1 6817347CD1
US-10-311-035-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAL, Preeti
AU-YOUNG, Janice
TRIBOULEY, Catherine M.
DELEGEANE, Angelo M.
BAUGHN, Mariah R.
NGUYEN, Danniel B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/10311035
Publication No. US20440023243A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YUE, Henry
APPLICANT: ELLIOTT, Vicki
APPLICANT: ELLIOTT, Vicki
APPLICANT: GANDHI, Ameena R.
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REDDY, Roopa
DAS, Depopriya
KEARNEY, Liam
KALLICK, Deborah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAWLA, Narinder K. YAO, Monigue G. LU, Dyung Aina M. ARVIZU, Chandra S. TANG, Y. Toom WALSH, Roderick T. AZIMZAI, Yalda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LU, Yan
RAMKUMAR, Jayalaximi
; NUMBER OF SEQ 1D NOS: 150
; SOFWARR: Patentin Ver. 2.1
; SEQ 1D NO 66
; LENGTH: 953
; TYPE: RRT
; ORPANISM: Homo sapiens
US-09-888-615-66
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HAFALIA, April
KHAN, Farrah A.
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US-10-311-035-21
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Sequence 277859, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF SINGENT SPATISATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 277859
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39176
LENGTH: 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.9%; Score 55; DB 12; Length 539; Best Local Similarity 65.0%; Pred. No. 2.1e+02; Matches 13; Conservative 1; Mismatches 2; Indels
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US-10-424-599-277859
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Clone ID: LIB3245-443-A8_FLI.pep
US-10-425-114-39176
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Best Local Similarity 73.39
Watches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                        APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Covalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Goreen, Steven E
APPLICANT: Cac, Yongwei
TITLE CAC, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-2153313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-4-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.9%; Score 55; DB 12; Length 240; Best Local Similarity 65.0%; Pred. No. 1.1e+02; Matches 13; Conservative 1; Mismatches 2; Indels
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US-10-425-114-40613
Sequence 40613, Application US/10425114
Fublication No. US20040034888A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Lou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Panels Acid Molecules and O
TITLE OF INVENTION: Nucleic Acid Molecules and O
TITLE OF INVENTION: Plants and Uses Thereof for File Reference: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 40613
LENGTH: 299
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 GHGRPPPLDRORPOOGPPRO 174
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                                            Publication No. US200400348881
                                                                     GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
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US-10-425-114-39176
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Length 52;

Indels

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ZIP: 53202-4108 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                 RESULT 1
US-09-252-991A-29332
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-29332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-925-237-4
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Sequence 30870, A
Sequence 24480, A
Sequence 79, Appl
Sequence 17072, A
Sequence 31760, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29332, A
Sequence 4, Appli
Sequence 2, Appli
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Sequence 31760, A
Sequence 29, Appl
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Sequence 27513, A
Sequence 27041, A
                                                             6, 2004, 15:56:34; Search time 24.9439 Seconds (Without alignments) 35.185 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38
Sequence 38
Sequence 38
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Sequence 2
Sequence 2
Sequence 6
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Sequence 2
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(Ggn2 6/ptodata/2/jaa/5A_COMB.pep:*
(Ggn2 6/ptodata/2/jaa/5B_COMB.pep:*
(Ggn2 6/ptodata/2/jaa/6A_COMB.pep:*
(Ggn2 6/ptodata/2/jaa/6B_COMB.pep:*
(Ggn2 6/ptodata/2/jaa/FB_COMB.pep:*
(Ggn2 6/ptodata/2/jaa/PCTUS_COMB.pep:*
(Ggn2 6/ptodata/2/jaa/PCTUS_COMB.pep:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-467-344A-38
US-09-252-991A-20316
US-09-252-991A-27513
US-09-252-991A-27041
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US-09-252-991A-24480
US-09-413-814-79
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US-09-252-991A-31760
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                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                                                                                                                                                                               389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 GGHPRPPRGRPQGPPQQ 17
                                              protein search, using sw
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Maximum DB seq length: 200000000
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Perfect score:
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No.
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28 53 51.0 799 4 US-09-252-991A-25652 Sequence 26622, A Sequence 2555, A Sequence 2555, A Sequence 2555, A US-09-252-991A-25595 Sequence 2555, A US-09-252-991A-25595 Sequence 2555, A US-09-252-991A-25595 Sequence 2555, A US-09-252-991A-25505 Sequence 2555, A US-09-252-991A-25505 Sequence 25, Appli 35 52 50.0 451 4 US-09-074-349-2 Sequence 2, Appli 36 52 50.0 452 1 US-07-937-609-16 Sequence 16, Appli 36 52 50.0 452 1 US-07-937-609-16 Sequence 16, Appli 37 52 50.0 452 1 US-07-937-609-16 Sequence 16, Appli 37 52 50.0 553 4 US-09-252-991A-32631 Sequence 26802, A US-09-252-991A-32631 Sequence 26802, A US-09-252-991A-26802 Sequence 26902, A US-09-252-991A-26802 Sequence 26902, A US-09-252-991A-26802 Sequence 26902, A US-09-252-991A-29074 Sequence 26902, A US-09-252-991A-29074 Sequence 26902, A US-09-252-991A-26808 Sequence 4, Appli 44 51 49.0 380 2 US-09-252-991A-26318 Sequence 26318, A US-09-252-991A-26318 Sequence 26318, A US-09-252-991A-26318 Sequence 26318, A US-09-252-991A-21709 Sequence 26318, A US-09-252-991A-21709
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ALIGNMEN

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RESULT 1

19.09-25-291A-29332

19.09-292-231 Application US/09252991A

19.09-292-232 Application US/09252991A

19.09-292-232 Application US/09252991A

19.09-292-232 Application US/09252991A

19.09-292-291A-29332

19.09-292-291A-29332

19.09-292-291A-29332

19.09-292-291A-29332

19.09-292-291A-29332

19.09-292-291A-2932

19.09-292-291A-29323

19.00-292-291A-29323

20.00-292-291A-29323

20.00-292-291A-29323

20.00-292-291A-29323

20.00-292-2924

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20.00-2024

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Sequence 30870, Application US/09252991A

Sequence 30870, Application US/09252991A

Parent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J.
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30870
LENGTH: 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: 05.09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

ERIOTH: 559
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Pred. No. 12;
0; Mismatches 3; Indels
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                                       Indels
               Best Local Similarity 57.1%; Pred. No. 1; Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24480, Application US/09252991A Patent No. 6551795
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US-09-413-814-79
; Sequence 79, Application US/09413814
                                                                                        1 GGH----PRPPRGRPQGPPQQ 17
                                                                                                                                       13 GGNQPQGPPPPGKPQGPPPQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.8%;
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Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 PRPPASRPPGPP 201
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Sequence 2, Application US/08925237
Sequence 2, Application US/08925237
Sequence 2, Application US/08925237
Partent No. 5981720;
GENERAL INFORMATION:
APPLICANT: Pan, Davin A.
TITLE OF INVENTION: Human Salivary Proteins And Fragments
TITLE OF INVENTION: Thereof Having Alpha-Glucosidase Inhibitory Activity
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kent Barta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 59.6%; Score 62; DB 2; Length 82; Local Similarity 57.1%; Pred. No. 0.69; see 12; Conservative 2; Mismatches 3; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,237
FILING DATE:
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Barta, Kent S:
REFERENCE/DOCKET NUMBER: 96429/9002
TELEPHONE: (608) 257-3501
TELEPHONE: (608) 283-275
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERESTICS:
LENGTH: 92 amino acids
mvor: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY. USA
ZIP. 53202-4108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,237
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT THORNATION:
NAME: Barta, Kent 8.
REGISTRATION NUMBER: 29,042
REPREMENCE/DOCKET NUMBER: 96429/9002
TELEPANICATION INFORMATION:
TELEPHONE: (608) 257-3501
TELEPHONE: (608) 283-275
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.6%; Score 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Kent Barta
STREET: 100 East Wisconsin Avenue
CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGH----PRPPRGRPQGPPQQ 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 124 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-925-237-4
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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Matches
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1999-02-18

PRIOR PELING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31760

LENGTH: 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KAINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: QERMINO, GREGORY
APPLICANT: OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSED CONVENTION: DALESCONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 4;
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENZYME CORPORATION ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/POCKET NUMBER: GEN4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1545 GRPRPPGRAPGPRO 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%;
Matches 10; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: FRAMINGHAM STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
STREET: ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APPLICANCE.

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US,09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SED ID NOS: 33142
EROGTH: 223
LENGTH: 223
                                                                                                                                                                                                                                                                                          APPLICANT: Wieller, Joachim
APPLICANT: Reichembach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DATE: D09/22535
FILE REFERENCE: PCT/US 99/22535
CURRENT APPLICATION NUMBER: U5/09/413,814
EARLIER APPLICATION NUMBER: DE 1989-10-07
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
LENGTH: 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.8%; Score 56; DB 3; Length 1213; 75.0%; Pred. No. 39;
                                                                               Gesellschaft fuer Biotechnologische Forschung mbH Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 4; Length 223;
Pred. No. 11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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US-09-252-991A-31760
; Sequence 31760, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17072, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.9%;
                                                                                                                                                                        APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Cougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
                                                                                                                              Beyer, Stefan
Bloecker, Helmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 75.0
Matches 9; Conservative
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GEORGE J. DAWSON
GEORGE G. SCHAUDER
SURESH M. DESAI
THOMAS P. LEBARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: 1L
                                                PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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      Gaps
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TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-B HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
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51.9%; Score 54; DB 4; Length 245;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 4; Indels
      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTRY: USA
ZIP: 60064-3500
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5527.PC.01
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
                                                                                                                                                                                                                                               JOHN N. SIMONS
JAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SUTASAN DESAN
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLALLATOR PROBLEM THEORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 708-938-2635
TELEFAX: 708-938-2633
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
TEMPORALION FOR SEQ ID NO: 38:
                                                                                                                                                                                   Sequence 38, Application US/08469260A
Patent No. 6451578
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 38, Application US/08488446
Patent No. 6558898
                                       2 GHPRPPRGRPQGPPQQ 17
                                                                                 4 GPSRTPSGQEQGPPQQ 19
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10; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                             US-08-469-260A-38
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US-08-488-446-38
  Matches
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Gaps
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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16;
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                                                                                                                                                                COUNTRY: UGA

ZIP: COUNTRY: UGA

ZIP: 60064-3500
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
FILING DATE:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
APPLICATION NUMBER: 33.207
REFERENCE/DOCKET NUMBER: 33.207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUTCATION INFORMATION:
TELEFRAK: 708-937-6365
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LEMETAL 245 aming acids
TELEFRACE CHARACTERISTICS:
                                                                                       D377/AP6D
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US-08-467-J...

Sequence 38, Applia...

Sequence 38, Applia...

Patent No. 6586568

GENERAL INFORMATION:

TAMI J. FILOT-KATIAS

GEORGE J. DAWSON

GEORGE G. SCHLAUDER

JUNEAH M. DESAI

THOMAS P. LERRY

JAMES C. ERKER

SHERI L. BUIJK

ISA K. MUSHAHWAR
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US-09-252-991A-27513
; Sequence 27513, Application US/09252991A
; Patent No. 6551795
                                                                              91 GHPGVVADTRLRQHRGRPAGPPER 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| || || :| || 270 GHPHPPDGRLRGHPR 284
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Matches 9; Conservative
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Job time : 24.9439 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Patent No. 6551795

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC AID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107126.136
CURRENT PEPTICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142

LENGTH: 291
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TITLE OF INVENTION: NOM-A, NON-B. NON-C, NON-D, NON-E HEPATITIS REAGENTS AND METHODS FOR THEIR USE
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                                                                                                                                                                    COUNTRY: UGA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DATA COMPA:
COMPUTER: DATA COMPA:
COMPUTER: DATA COMPA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION NUMBER: 08/424,550
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: 08/424,550
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: PORRMERK! PRISCILLA E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
51.9%; Score 54; DB 4; Length 391;
Best Local Similarity 45.8%; Pred. No. 24;
Matches 11; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                            CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
SITY: ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: 1L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33.207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.9%; Score 54; 69.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 HPRPPEPRPSGLP 134
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Best Local Similarity 69.2°
Matches 9; Conservative
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                                              NUMBER OF SEOUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-20316
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27041, Application US/09252991A

Retent No. 6551795

Retent No. 6551795

Retent No. 6551795

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PELLOATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

EROTH: 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.9%; Score 54; DB 4; Length 422; 64.3%; Pred. No. 26; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 4; Length 453; Pred, No. 27; 2; Mismatches 4; Indels
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